

Tue Dec 10 10:51:32 2002

us-09-880-457-1_COPY_486_746.rml

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:19 : Search time 15.2491 Seconds
(without alignments)
5249.015 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atggcaatccgcagcgtcag.....gtaattgagatcattcac 261Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Issued Patents, NA.*
1: /cgn2_6/prodata/1/lna/5A.COMB.seq.*
2: /cgn2_6/prodata/1/lna/5B.COMB.seq.*
3: /cgn2_6/prodata/1/lna/6A.COMB.seq.*
4: /cgn2_6/prodata/1/lna/6B.COMB.seq.*
5: /cgn2_6/prodata/1/lna/PCITUS.COMB.seq.*
6: /cgn2_6/prodata/1/lna/Backfiles1.seq.*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121.2	46.4	954	US-08-996-139-12	Sequence 12, Appl
2	121.2	46.4	954	US-08-995-659-12	Sequence 12, Appl
3	121.2	46.4	954	US-09-215-649A-12	Sequence 12, Appl
4	121.2	46.4	954	US-09-577-780-12	Sequence 3, Appl
5	121.2	46.4	2271	US-09-052-521C-3	Sequence 10, Appl
6	95.6	36.6	1630	US-08-996-139-10	Sequence 10, Appl
7	95.6	36.6	1630	US-08-995-659-10	Sequence 10, Appl
8	95.6	36.6	1630	US-09-215-649A-10	Sequence 10, Appl
9	95.6	36.6	1630	US-09-577-780-10	Sequence 10, Appl
10	95.6	36.6	2191	US-08-989-362-1	Sequence 6, Appl
11	95.6	36.6	2295	US-08-842-842-1	Sequence 1, Appl
12	95.6	36.6	2295	US-09-052-521C-1	Sequence 22, Appl
13	29.8	11.4	271	US-09-003-574-22	Sequence 22, Appl
14	29.8	11.4	689	US-09-003-574-20	Sequence 20, Appl
15	29.8	11.4	689	US-09-003-574-21	Sequence 21, Appl
16	29.8	11.4	804	US-09-003-574-21	Sequence 21, Appl
17	29.8	11.4	804	US-09-003-574-21	Sequence 1, Appl
18	29.8	11.4	1299	US-08-463-262A-1	Sequence 1, Appl
19	29.8	11.4	1299	US-08-463-989-1	Sequence 1, Appl
20	29.8	11.4	1299	US-09-003-574-1	Sequence 1, Appl
21	29.8	11.4	1299	US-09-003-574-1	Sequence 33, Appl
22	29.8	11.4	2028	US-09-003-574-33	Sequence 32, Appl
23	29.8	11.4	2028	US-09-003-574-32	Sequence 32, Appl
24	29.8	11.4	2032	US-09-003-574-32	Sequence 30, Appl
25	29.8	11.4	2032	US-09-003-574-30	Sequence 30, Appl
26	29.8	11.4	2076	US-09-003-574-30	Sequence 30, Appl
27	29.8	11.4	2076	US-09-003-574-30	Sequence 30, Appl

28	29.8	11.4	2076	US-09-003-570-30	Sequence 30, Appl
29	29.8	11.4	2126	US-08-463-262A-2	Sequence 2, Appl
30	29.8	11.4	2126	US-08-463-989-2	Sequence 2, Appl
31	29.8	11.4	2126	US-09-003-574-2	Sequence 2, Appl
32	29.8	11.4	2126	US-09-003-570-2	Sequence 29, Appl
33	29.8	11.4	2292	US-09-003-574-29	Sequence 29, Appl
34	29.8	11.4	2292	US-09-003-570-29	Sequence 47, Appl
35	29.4	11.3	1461	US-07-824-247-47	Sequence 7, Appl
36	29.4	11.3	1461	US-08-142-473A-7	Sequence 7, Appl
37	29.4	11.3	1461	US-08-463-523B-9	Sequence 7, Appl
38	29.4	11.3	1461	US-08-463-203A-7	Sequence 7, Appl
39	29.4	11.3	1461	US-08-463-203A-7	Sequence 7, Appl
40	29.4	11.3	1461	US-08-470-204A-47	Sequence 12, Appl
41	29.4	11.3	1461	US-08-926-522-12	Sequence 12, Appl
42	29.4	11.3	804	US-09-003-574-21	Sequence 21, Appl
43	29	11.1	804	US-09-003-570-21	Sequence 21, Appl
44	29	11.1	804	US-09-003-570-21	Sequence 21, Appl
45	29	11.1	1299	US-08-463-262A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 1..951
US-08-996-139-12

Query Match 46.4%; Score 121.2; DB 3; Length 954;
Best Local Similarity 74.8%; Pred. No. 1.3e-34;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCTGACGCTGACGCTTCACTCATCTGTTATTAATACATCAATATCCATGAG 63
DB 473 GCAAGTTGAAGCTGACGCTTTGCTCATCTCATTAATGCAACGACATCCATCTG 532
QY 64 GCT--CATAAAGAGTCTTTCTTGTGAAACATGACCAAGATTGGGCAAGCTTCCA 121
DB 533 GTTCCCATTAAGTGTGCTGTCTGTGTAACATGATCGGGGTTGGGCCAAGATCTCCA 592
QY 122 ACATGACTTTGACGACGGAAGAACTAAGTCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTTACGAAATGAAACTAATAGTATATGAGATGCTTTATTACCTGTATG 652
QY 176 CCGACATTTGCTGACATCGGCTTAACCTGACGACGCTTAACCTGACGACCTTACG 235
DB 653 CCAACATTTGCTTTCGACATCATGAACTTCAGAGACCTTACAGATATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 2

US-08-995-659-12
Sequence 12, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 1..951
US-08-995-659-12

Query Match 46.4%; Score 121.2; DB 4; Length 954;
Best Local Similarity 74.8%; Pred. No. 1.3e-34;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCTGACGCTGACGCTTCACTCATCTGTTATTAATACATCAATATCCATGAG 63
DB 473 GCAAGTTGAAGCTGACGCTTTGCTCATCTCATTAATGCAACGACATCCATCTG 532
QY 64 GCT--CATAAAGAGTCTTTCTTGTGAAACATGACCAAGATTGGGCAAGCTTCCA 121
DB 533 GTTCCCATTAAGTGTGCTGTCTGTGTAACATGATCGGGGTTGGGCCAAGATCTCCA 592
QY 122 ACATGACTTTGACGACGGAAGAACTAAGTCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTTACGAAATGAAACTAATAGTATATGAGATGCTTTATTACCTGTATG 652
QY 176 CCGACATTTGCTGACATCGGCTTAACCTGACGACGCTTAACCTGACGACCTTACG 235
DB 653 CCAACATTTGCTTTCGACATCATGAACTTCAGAGACCTTACAGATATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 3

US-09-215-649A-12
Sequence 12, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

1

RESULT 5
US-09-052-521C-3

Query Match	46.48;	Score 121.2;	DB 4;	Length 2271.
Best Local Similarity	74.88;	Pred. No. 2.1e-34;		
Matches 181; Conservative				

	4	GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTAATAAATAAA	8; Gaps	2;
--	---	--	---------	----

[illegible]

RESULT 6
US-08-996-139-10
; Sequence 10, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION.

APPLICANT: Galbert, Latent M.
APPLICANT: Marakovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIORITY:

APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064, 67
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813, 509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772, 330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)567-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE:

ORIGINAL SOURCE: ORGANISM: Mus

IMMEDIATE SOURCE:
LIBRARY:
OF:

CLONE:	RANKL
FEATURE:	
NAME/KEY:	CDC

LOCATION: 3..884
08-996-139-10

Query Match	36.6%;	Score 95.6;	DB 3;	Length 1630;
Best Local Similarity	68.28;	Pred. No. 4.2e-25;		
Matches 165;	Conservative			

	Mismatches	69;	Indels	8;	Gaps	2
--	------------	-----	--------	----	------	---

405 GGCAGCCTGAGGCCAGCCATTTCACACCTCATTACCATCAATATCCCATGA 62

63 GG--CTCATAAAGAGTCTTCTTCTTGGAACATGACCAACAGTTGGGCAACCTGCTCC 464
 ||| |||||
 465 GCTTCTTCTTCTTCTTCTTGGAACATGACCAACAGTTGGGCAACCTGCTCC 466

121 AACATGACTTTCGATTCCT 524

|||||GAGCAACGGAAACTAAGACTCA-----AAGCATTATTTACCGGAAAT 174
525 AACATGACGTTTAAGCAACCGGAATACTT|||||||

175 GCCGACATTGGCTTCGACATCGCCTAACCTCAAGCCGCCTT
|||||
|||

584

585 GCCAACATTTGCTTCGGCATCATGAACATCGGAGCGTCTACTACGCTTT
TAA TTA GGC CCA AGC CCA CTCT CGA GAC CTT CAG

235 CT 236
11
645 CT 646

PLT 7
8-995-659-10

Sequence 10, Application US/08995659
tent No. 6242213
GENERAL INFORMATION

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent

QY 3 GGCAATCTGACGCTGACGCTTCAACATCTTTATTATACATCAATATCCATGA 62
Db 405 GGCAAGCTGAGGCCGACGCTTTCACACCTCAACATCATCTGCGACATCCCATCG 464
QY 63 GG--CTCATTAAGACGATCTTTCTTTGGAACATACCAAGATTTGGGCAACGCTCC 120
Db 465 GGTTCCTCATTAAGTACCTCTCTCTTGTGACCATGAGGCTGGCCCAAGATCTCT 524
QY 121 AACATGACTTTGACGACGAAAGTAACTAGTCA-----AAGCATTTATTACCGGAT 174
Db 525 AACATGACGTTAAGCAAGGAAAGTAACTAGGTTTAAACAGATGCTTCTATTACCTGAC 584
QY 175 GCGCAGATTTGCTCTGACATCGCTTAACCTGACGAGGCTTACCTGACGACCTTCAG 234
Db 585 GCGAAGCATTTGCTTGGCATCATGAAACATCGGAGACGCTTACCTGACGACTTCTCAG 644
QY 235 CT 236
Db 645 CT 646

RESULT 9

US-09-577-780-10

Sequence 10, Application US/09577780
Patent No. 6419929

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Calibert, Laurent

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WACOUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/577,780

FILING DATE: 24-May-2000

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: <unknown>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:LIBRARY: <unknown>
CLONE: RANKL
FEATURE:NAME/KEY: CDS
LOCATION: 3..884

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-577-780-10

Query Match

Best Local Similarity 36.6%; Score 95.6; DB 4; Length 1630;
Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps 2;

QY 3 GGCAATCTGACGCTGACGCTTCAACATCTTTATTATACATCAATATCCATGA 62
Db 405 GGCAAGCTGAGGCCGACGCTTTCACACCTCAACATCATCTGCGACATCCCATCG 464
QY 63 GG--CTCATTAAGACGATCTTTCTTTGGAACATACCAAGATTTGGGCAACGCTCC 120
Db 465 GGTTCCTCATTAAGTACCTCTCTCTTGTGACCATGAGGCTGGCCCAAGATCTCT 524
QY 121 AACATGACTTTGACGACGAAAGTAACTAGTCA-----AAGCATTTATTACCGGAT 174
Db 525 AACATGACGTTAAGCAAGGAAAGTAACTAGGTTTAAACAGATGCTTCTATTACCTGAC 584
QY 175 GCGCAGATTTGCTCTGACATCGCTTAACCTGACGAGGCTTACCTGACGACCTTCAG 234
Db 585 GCGAAGCATTTGCTTGGCATCATGAAACATCGGAGACGCTTACCTGACGACTTCTCAG 644
QY 235 CT 236
Db 645 CT 646

RESULT 10

US-08-989-362-1

Sequence 1, Application US/08989362

Patent No. 6242586

GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.

TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESS: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,362

FILING DATE: 12-DEC-1997

CLASSIFICATION: 56

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,846

FILING DATE: 13-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0686

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)496-1204

TELEFAX: (650)496-1204

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2191 base pairs
TYPE: nucleic acid

36.68; Score 95.6; DB 2; Length 2295;

Query Match	36.6%;	Score 95.6;	DB 4;	Length 2295;
Best Local Similarity	68.2%;	Pred. No. 5.1e-25;		
Matches 165;	Conservative	0;	Mismatches 69;	Indels 8;
				Gaps 2;
QY	3	GGCAATCTGAGCTCAGGCTTCACACTCATCTTGTATTAACTACCAATCATATGCCATGA	62	
Db	626	GGCAAGCTGAGGCCAGCCATTTCACACCTCACCACCTAAATGCTGCCAGATGCCATCG	685	
QY	63	GG--CCTCATAAACGAGTCTTCTCTCTTGGAACATGACCAAGATTGGGCAACGCTCC	120	
Db	686	GGTTCCCATTAATCACTCTGTCTCTTGTGTCACAGATCGAGGTGGGCCAATCTCT	745	
QY	121	AACATGACTTTCAGCAACGGAAACCTAAGACA-----AAGCATTTATTATCCGGAA	174	
Db	746	AACATGACGTTAAGCAACGGAAACCTTAAGGTTAAOCMAAGATGGCTTCAATACCTGTAC	805	
QY	175	GCCACACTTTGCTCTGCAATGCGGTAACTCAGCAGGCGCTAACTGTGAGGACCTTAG	234	
Db	806	GCCAACTTTGCTTTCGCGATCAATGAAGACATCGGAAAGCTTACTTACAGACATATTTCAG	865	
QY	235	CT 236		
Db	866	CT 867		

RESULT 13

US-09-003-574-22

Sequence 22, Application US/09003574

Patent No. 6265198

GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia Ann

APPLICANT: Frank, Glenn R.

TITLE OF INVENTION: NOVEL PARASITE ASTACIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESSES:

ADDRESS: SHERIDAN ROSS P.C.

STREET: 1700 LINCOLN ST., SUITE 3500

CITY: DENVER

STATE: CO

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,574

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-21-1-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 271 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-003-574-22

Query Match

Best Local Similarity 11.4%; Score 29.8; DB 4; Length 271;

Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db

26 AACGATCTGTATTATACCATCATATCCCATGAGCTCATAAACGAGTCTT 82

70 AAATCATATTTTATTATATACCAATATTCATCAAGCGTTGGAACATTTTT 126

RESULT 14

US-09-003-570-22

Sequence 22, Application US/09003570

Patent No. 6281345

GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia Ann

APPLICANT: Frank, Glenn R.

TITLE OF INVENTION: NOVEL PARASITE ASTACIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESSES:

ADDRESS: SHERIDAN ROSS P.C.

STREET: 1700 LINCOLN ST., SUITE 3500

CITY: DENVER

STATE: CO

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,570

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-21-4-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 271 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-003-570-22

Query Match

Best Local Similarity 11.4%; Score 29.8; DB 4; Length 271;

Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db

26 AACGATCTGTATTATACCATCATATCCCATGAGCTCATAAACGAGTCTT 82

70 AAATCATATTTTATTATATACCAATATTCATCAAGCGTTGGAACATTTTT 126

RESULT 15

US-09-003-574-20

Sequence 20, Application US/09003574

Patent No. 6265198

GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia Ann

APPLICANT: Frank, Glenn R.

TITLE OF INVENTION: NOVEL PARASITE ASTACIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESSES:

ADDRESS: SHERIDAN ROSS P.C.

STREET: 1700 LINCOLN ST., SUITE 3500

CITY: DENVER

STATE: CO

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,574

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-21-1-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 689 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

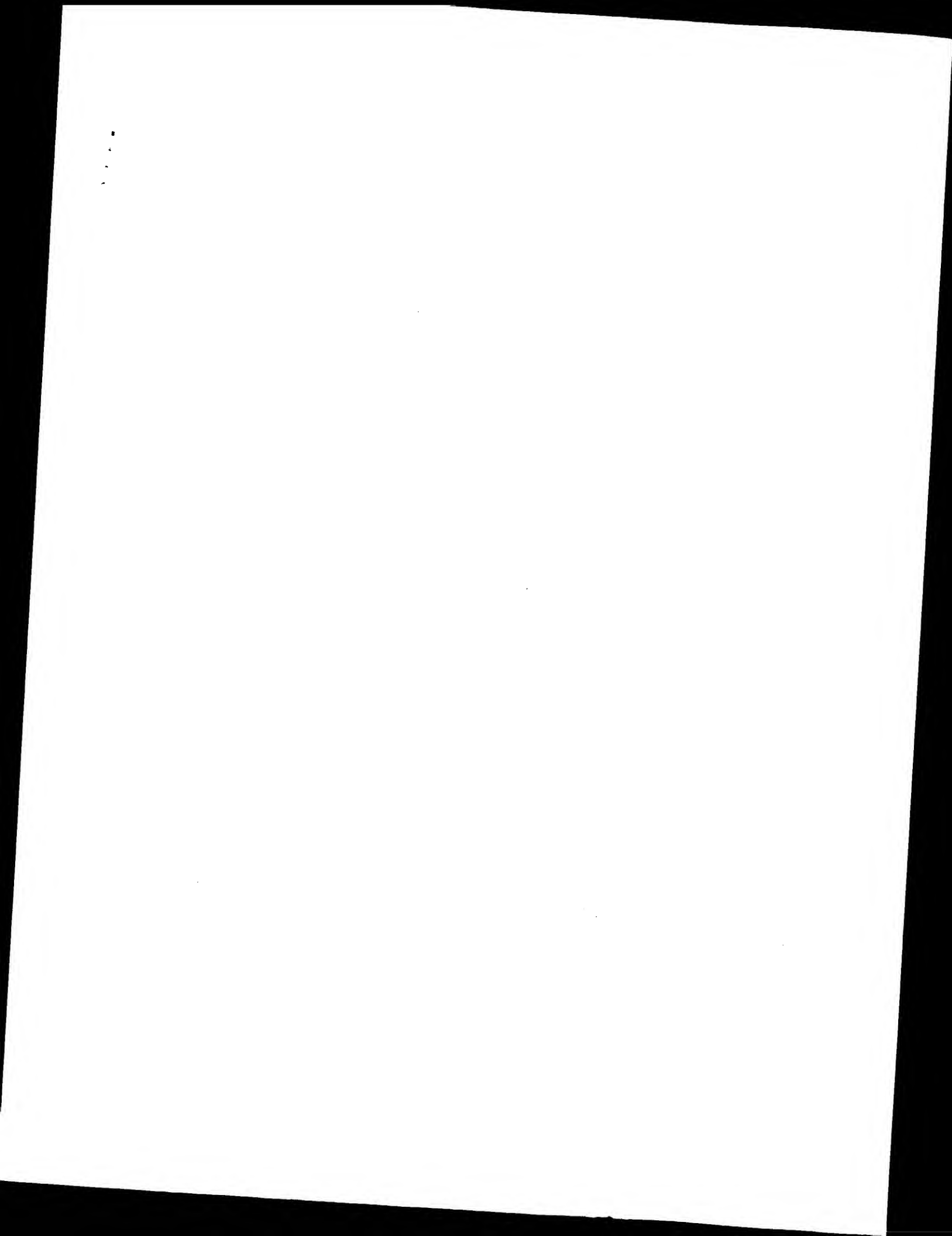
Tue Dec 10 10:51:32 2002

us-09-880-457-1_copy_486_746.rni

US-09-003-574-20

Query Match 11.4%; Score 29.8; DB 4; Length 689;
 Best Local Similarity 70.2%; Pred. No. 0.34; 17; Indels 0; Gaps 0;
 Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 Oy 26 AACTCATCTTGTATPAATACATCAATATCCCATGAGCTCATTAACGAGCTTT 82
 60 AAATCATATTTTATTTATTAATACAAATATTCATCAAGCCGTTGGAACAATTTT 116

Search completed: December 8, 2002, 17:28:26
 Job time : 22.2491 secs



Tue Dec 10 19:51:27 2002

us-09-880-457-1.rn1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 8, 2002, 15:56:19 : Search time 67.8321 Seconds
(without alignments)
5249.015 Million cell updates/sec

Title: US-09-880-457-1
Perfect score: 1161
Sequence: 1 aaagaaggaataatcaaga.....taataaagaaggaataatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues 882724

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCRTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	10.9	954	3	US-08-996-139-12 Sequence 12, Appl
2	126	10.9	954	4	US-08-995-659-12 Sequence 12, Appl
3	126	10.9	954	4	US-09-215-649A-12 Sequence 12, Appl
4	126	10.9	954	4	US-09-577-780-12 Sequence 3, Appl
5	126	10.9	2271	4	US-09-052-521C-3 Sequence 10, Appl
6	97	8.4	1630	3	US-08-996-139-10 Sequence 10, Appl
7	97	8.4	1630	4	US-08-995-659-10 Sequence 10, Appl
8	97	8.4	1630	4	US-09-215-649A-10 Sequence 10, Appl
9	97	8.4	1630	4	US-09-577-780-10 Sequence 1, Appl
10	97	8.4	2191	4	US-08-989-362-1 Sequence 6, Appl
11	97	8.4	2295	2	US-08-842-842-6 Sequence 1, Appl
12	97	8.4	2295	2	US-08-842-842-6 Sequence 14, Appl
13	53	4.6	7218	1	US-08-052-521C-1 Sequence 1, Appl
14	37	3.2	289	4	US-08-232-463-14 Sequence 1, Appl
15	37	3.2	289	4	US-09-007-005-17 Sequence 1, Appl
16	37	3.2	289	4	US-09-244-796-17 Sequence 10, Appl
17	37	3.2	99500	4	US-09-198-409-1 Sequence 1, Appl
18	37	3.2	99500	3	US-09-335-409-1 Sequence 1, Appl
19	34.6	3.0	68750	4	US-09-568-102-1 Sequence 1, Appl
20	34.6	3.0	68750	4	US-09-568-102-1 Sequence 1, Appl
21	34.6	3.0	68750	4	US-09-567-969-1 Sequence 1, Appl
22	34.6	3.0	68750	4	US-09-568-480-1 Sequence 1, Appl
23	34.6	3.0	68750	4	US-09-568-486-1 Sequence 1, Appl
24	34.6	3.0	68750	4	US-09-568-472-1 Sequence 1, Appl
25	33.8	2.9	1280	4	US-09-567-899-1 Sequence 3, Appl
26	33.8	2.9	1280	4	US-08-027-986-3 Sequence 4, Appl
27	33.6	2.9	1356	4	US-08-952-736A-1 Sequence 2, Appl

28	33.6	2.9	71989	4	US-09-443-501A-2 Sequence 2, Appl
29	32.8	2.8	2040	1	US-08-599-252-103 Sequence 103, App
30	32.8	2.8	2040	5	PCT-US96-06352-103 Sequence 103, App
31	32.8	2.8	2040	5	PCT-US96-06583-103 Sequence 10, Appl
32	32.4	2.8	1314	2	US-08-868-577-10 Sequence 10, Appl
33	32.4	2.8	1315	2	US-08-671-320-10 Sequence 18, Appl
34	32.4	2.8	3341	2	US-08-868-577-18 Sequence 1, Appl
35	32.2	2.8	1483	4	US-09-262-749-1 Sequence 1, Appl
36	32.2	2.8	1553	3	US-09-022-669-1 Sequence 1, Appl
37	32.2	2.7	44453	4	US-09-603-567-1 Sequence 5, Appl
38	31.8	2.7	521	4	US-09-146-053-5 Sequence 245, App
39	31.6	2.7	521	4	US-08-991-789A-245 Sequence 245, App
40	31.6	2.7	521	4	US-09-062-451-245 Sequence 245, App
41	31.6	2.7	521	4	US-09-598-326-245 Sequence 1, Appl
42	31.6	2.7	2169	1	US-08-379-496-1 Sequence 32, Appl
43	31.4	2.7	248	4	US-09-007-005-32 Sequence 32, Appl
44	31.4	2.7	248	4	US-09-244-796-32 Sequence 3, Appl
45	31.4	2.7	277	4	US-09-007-005-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galbert, Laurent
APPLICANT: Markovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

NAME/KEY:	CDS
LOCATION:	1..951
US-08-996-139-12	

Query Match	10.98;	Score 126;	DB 3;	Length 954;
Best Local Similarity	72.68;	Pred. No. 1.4e-31;		
Matches 193;	Conservative			

[illegible]

RESULT 2
US-08-995-659-12
; Sequence 12, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

LENGTH: 954 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: 14

MOLECULE TYPE: CDNA
HYPOTHETICAL

ANTI-SENSE: NO

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
LIBRARY:

CLONE: hurankl (full length)

FEATURE:

NAME/KEY:	CDS
LOCATION:	1..951
US-08-995-659-12	

Query Match	10.98;	Score 126;	DB 4;	Length 954
Best Local Similarity	72.68;	Pred. No. 1.4e-31;		
Matches 193;	Conservative	0;	Microbial	

		mismatches	65;	Indels	8;	Gaps	
Oy	465 CAGGAGAATATTGTCTAAGAAATGGCAATCCTGACGCTCAGCCCTTCACAACCTCATCTGTTA						2
Db	449 CATGTTTAGATCTCGGCCAACGAGGAAGTTTAACTCAGCTTTTGCTCTACACTA						
Oy	525 TTAATACCATCAATATCCCATGTAGGCT--CATMAACGAGTCTTCTCTTTGGAACATG						
Db	509 TTATATGCACCAGCATCTCCATCTGGTCCCAAATAAGTAGTGTGTCTCTTGGTACCATG						
Oy	583 ACCAATATTGGGCAAAACGCTTCCAACATGACTTGGAGAACGGAATTAAGAGTCA---						
Db	569 ATCGGGGTTGGGCGCAAGATCTCCACATCATGACTTTAGCAATAGAAAACTATATTATTC						
Oy	640 ---AAGCATTATTTACCAGATGCGGCAATTGCTCTCGACATCGGCTAATCCGCACAG						
Db	629 AAGATGGCTTTTATATTACCTGTATGCCAAACTTTTCTTTCACATCATGAAACCTTCAGGAG						
Oy	697 GCCTACTCTTCGACAGACTTCAGCTA 722						
Db	689 ACCTAGCTACAGATATCTTCACACTA 714						

RESULT 3
 US-09-215-649A-12
 Sequence 12, Application US/09215649A
 Patent No. 62271349
 GENERAL INFORMATION:
 APPLICANT: Anderson, Dirk M.
 Galiberti, Laurent
 Maraskovsky, Eugene
 TITLE OF INVENTION: Receiver
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5

```

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-215-649A-12

Query Match      10.9%; Score 126; DB 4; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.4e-31;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAAATGTTGCTTAAGATGCAATGCTGAGCTGCTCAACATCTTGTTA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 CAGGTGTAAGTCGCGCAAGAGAGAGAGCTTGAAGCTCAGCTTTGCTCATCTCACTA 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAAGAGCTTTCTTTGGAACATG 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 509 TTATATGCACGACATCCCATCTGCTCCATTAAGTAGAGTCTGCTCTTGATACCATG 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 583 ACCAAGATTGGGCAACAGCTCTCCACATGACTTTGACACAGGAAACTAAGATCA--- 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 569 ATCGGGGTGGGCCAAGATCTCCACATGACTTTTACCAATGGAAGAACTAATGTTATC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 ---AAGCATTTTATACCGAATGCGACATTTGCTCTCGACATCGGTAACCTCAGCAG 696
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 629 AGGATGCGTTTATATCTGATGATCCCAAGATTTGCTTTGACATCAGAAACTCAGAG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 697 GCCTAACTCTGCAGACCTTCAGCTA 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 689 ACCTAGTACAGAGATATCTTCACTA 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-09-577-780-12
Sequence 12, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galbert, Laurent
Markovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

```

```

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-577-780-12

Query Match      10.9%; Score 126; DB 4; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.4e-31;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAAATGTTGCTTAAGATGCAATGCTGAGCTGCTCAACATCTTGTTA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 CAGGTGTAAGTCGCGCAAGAGAGAGAGCTTGAAGCTCAGCTTTGCTCATCTCACTA 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAAGAGCTTTCTTTGGAACATG 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 509 TTATATGCACGACATCCCATCTGCTCCATTAAGTAGAGTCTGCTCTTGATACCATG 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 583 ACCAAGATTGGGCAACAGCTCTCCACATGACTTTGACACAGGAAACTAAGATCA--- 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 569 ATCGGGGTGGGCCAAGATCTCCACATGACTTTTACCAATGGAAGAACTAATGTTATC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 ---AAGCATTTTATACCGAATGCGACATTTGCTCTCGACATCGGTAACCTCAGCAG 696
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 629 AGGATGCGTTTATATCTGATGATCCCAAGATTTGCTTTGACATCAGAAACTCAGAG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 697 GCCTAACTCTGCAGACCTTCAGCTA 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 689 ACCTAGCTACAGAGTATCTTCAACTA 714

RESULT 5
US-09-052-521C-3

Sequence 3, Application US/09052521C
Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.

TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors

FILE REFERENCE: A-451Biv

CURRENT APPLICATION NUMBER: US/09/052,521C

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 08/880,855

PRIOR FILING DATE: 1997-06-23

PRIOR APPLICATION NUMBER: 08/842,842

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 2271

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: CDS

LOCATION: (185)..(1135)

US-09-052-521C-3

Query Match

Best Local Similarity 10.9%; Score 126; DB 4; Length 2271;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

```

QY 465 CAGAGAGAGTATTGCTAAGAGGCAATCCTGACGCTCAGCTCACTCATCTGTTA 524
Db 633 CAGGTGATGATCTGGCCAGAGAGCAAGCTGAGCTCAGCTTGGCTCATCTCACTA 692
QY 525 TTATACCATCAATATCCATGAGGCT--CATAAAGCATCTTCTCTGGAACATG 582
Db 693 TTATGCGACGCAATCCATCTGTTCCATTAAGTGTCTCTCTGTTGTTACCATG 752
QY 583 ACCAAGTTGGGCAACGCTCTCCACATGACTTTCAGCAAGGAAACTAAGATCA--- 639
Db 753 ATCGGGGTGGGCGCAAGATCTCCACATGACTTTTGAACAATGAAACTAATGTTAA 812
QY 640 ---AAGGCATTTATTCACCGAATCGGACATTCCTGACATGCGGTAACCTGACAG 696
Db 813 AGATGCGCTTTTATTAAGCTGATGCGCAACATTTGCTTGCACATCATGAACCTCAGAG 872
QY 697 GCCTAAGCTGCGAGACCTTCAGCTA 722
Db 873 ACCTAGCTACAGAGTATCTTCAACTA 898

```

RESULT 6

US-08-996-139-10

Sequence 10, Application US/08996139

Patent No. 6017729

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mus musculus

IMMEDIATE SOURCE:

LIBRARY:

CLONE: RANL

FEATURE:

NAME/KEY: CDS

LOCATION: 3..884

US-08-996-139-10

Query Match

Best Local Similarity 8.4%; Score 97; DB 3; Length 1630;
Matches 170; Conservative 0; Mismatches 75; Indels 8; Gaps 2;

```

QY 477 TTGCTAAGAAATGGCAATCTGACGCTCAGCTCAACTCATCTGTTATTAATACATCA 536
Db 394 TGGCCACGAGGCAAGGCTGAGGCCCATTTGCACACCTCACCATCAATGCTGCCA 453
QY 537 ATATCCCATGAGG--CTCATAAACGAGTCTTCTTCTTGGAAACATGACCAAGATTGG 594
Db 454 GCATCCCATGCGGTTCCCATTAAGTCACTCTGCTCTTGGTACACGATCGAGGCTGG 513
QY 595 CAACGCTCTCCACATGACTTTCAGCAACGAAACTAAGATCA-----AAGGCAATT 648
Db 514 CCAAGATCTTAAACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCT 573
QY 649 ATTACCGGAATGCGGCAATTCCTGACATGCGGTAACCTGACGAGGCTTACTGTCG 708
Db 574 ATTACCTGTACCCCAATTTGCTTGGCATCATGAACATCGGAGGCTACTACAG 633
QY 709 AGGACCTTCAGCT 721
Db 634 ACTATCTTCAGCT 646

```

RESULT 7

US-08-995-659-10

Sequence 10, Application US/08995659

Patent No. 6242213

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

```

1  APPLICANT: Maraskovsky, Eugene
2  TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
3  NUMBER OF SEQUENCES: 19
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Immunex Corporation, Law Department
6  STREET: 51 University Street
7  CITY: Seattle
8  STATE: WA
9  COUNTRY: USA
10 ZIP: 98101
11
12 COMPUTER READABLE FORM:
13
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: Apple Power Macintosh
16 OPERATING SYSTEM: Apple Operating System 7.5.5
17 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/995,659
20 FILING DATE: 22 DECEMBER 1997
21
22 CLASSIFICATION:
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: USSN 60/064,671
26 FILING DATE: 14 OCTOBER 1997
27
28 CLASSIFICATION:
29
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: USSN 08/813,509
32 FILING DATE: 07 MARCH 1997
33
34 CLASSIFICATION:
35
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: USSN 08/772,330
38 FILING DATE: 23 DECEMBER 1996
39
40 CLASSIFICATION:
41
42 ATTORNEY/AGENT INFORMATION:
43 NAME: Perkins, Patricia Anne
44 REGISTRATION NUMBER: 34,693
45 REFERENCE/DOCKET NUMBER: 2852-A
46 TELECOMMUNICATION INFORMATION:
47 TELEPHONE: (206)587-0430
48 TELEFAX: (206)233-0644
49 INFORMATION FOR SEQ ID NO: 10:
50
51 SEQUENCE CHARACTERISTICS:
52 LENGTH: 1630 base pairs
53 TYPE: nucleic acid
54 STRANDEDNESS: single
55 TOPOLOGY: linear
56 MOLECULE TYPE: cdna
57 HYPOTHETICAL: NO
58 ANTI-SENSE: NO
59
60 ORIGINAL SOURCE:
61 ORGANISM: Mus musculus
62 IMMEDIATE SOURCE:
63 LIBRARY:
64
65 CLONE: RANKL
66
67 FEATURE:
68 NAME/KEY: CDS
69 LOCATION: 3..884
70
71 US-08-995-659-10

```

Query Match	8.4%;	Score 97;	DB 4;	Length 1630;
Best Local Similarity	67.2%;	Pred. No. 8e-22;		
Matches 170;	Conservative 0;	Mismatches 75;	Indels 8;	Gaps 2

QY	477	TTGCTAAGATGGCAANTCCTGACGCTCAGCCCTTCAACTCATCTTGTTATTAATATACATCA	536
Db	394	TGGCCACAGCAGGACGAGCTGAGGCCAGCCATTGGCAACCTCAACATCATGCTGCCA	453
QY	537	ATATCCCATGAG--CTATATAACGAGCTCTTCTTTGGAAACATGACCAAGATTGGG	594
Db	454	GCATCCCATGGGGTCCCATTAAGTCACACTCTGTCTCTTGTATCCACGATCAGAGCTGGG	513
QY	595	CAAAAGTTCGAACATGACTTTCAGCAACGGAAACTAAGATTCA-----AAGGATTT	648
Db	514	CCAAAGATCTTACATGACGTTAAGCAACGGAAAACCTAAGGCTTTAACCAAGATGGCTTCT	573

QY	649	ATTACGGGAATGCCGACATTTGCTTCGACATCCGTAATCCGACAGGGCTAAATCTGC	708
Db	574	ATTACCTGTACGCCAACATTTCTTTGGCATCTGAAACATCGGANAAGCTTACTCAG	633
QY	709	AGGACCTTCACCT	721
Db	634	ACTATCTTCACCT	646

```

      RESULT 8
      US-09-215-649A-10
      : Sequence 10, Application US/09215649A
      : Patent No. 6271349
      :
      : GENERAL INFORMATION:
      :   APPLICANT: Anderson, Dirk M.
      :             Galibert, Laurent
      :             Maraszkovsky, Eugene
      :   TITLE OF INVENTION: Receptor Activator of NF-kappaB
      :   NUMBER OF SEQUENCES: 19
      :   CORRESPONDENCE ADDRESS:
      :     ADDRESS: Immunex Corporation, Law Department
      :     STREET: 51 University Street
      :     CITY: Seattle
      :     STATE: WA
      :     COUNTRY: USA
      :     ZIP: 98101
      :
      : COMPUTER READABLE FORM:
      :   MEDIUM TYPE: Floppy disk
      :   COMPUTER: Apple Power Macintosh
      :   OPERATING SYSTEM: Apple Operating System 7.5.5
      :   SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
      :   CURRENT APPLICATION DATA:
      :     APPLICATION NUMBER: US/09/215,649A
      :     FILING DATE: 17-Dec-1998
      :     CLASSIFICATION: <unknown>
      :   PRIOR APPLICATION DATA:
      :     APPLICATION NUMBER: 08/996,139
      :     FILING DATE: <unknown>
      :     APPLICATION NUMBER: USSN 08/813,509
      :     FILING DATE: 07 MARCH 1997
      :     APPLICATION NUMBER: USSN 08/772,330
      :     FILING DATE: 23 DECEMBER 1996
      :   ATTORNEY/AGENT INFORMATION:
      :     NAME: Perkins, Patricia Anne
      :     REGISTRATION NUMBER: 34 693
      :     REFERENCE/DOCKET NUMBER: 2851-A
      :   TELECOMMUNICATION INFORMATION:
      :     TELEPHONE: (206)587-0430
      :     TELEFAX: (206)233-0644
      :
      : INFORMATION FOR SEQ ID NO: 10:
      :   SEQUENCE CHARACTERISTICS:
      :     LENGTH: 1630 base pairs
      :     TYPE: nucleic acid
      :     STRANDEDNESS: single
      :     TOPOLOGY: linear
      :   MOLECULE TYPE: cDNA
      :   HYPOTHETICAL: NO
      :   ANTI-SENSE: NO
      :   ORIGINAL SOURCE:
      :     ORGANISM: Mus musculus
      :   IMMEDIATE SOURCE:
      :     LIBRARY: <unknown>
      :     CLONE: RANKL
      :
      : FEATURE:
      :   NAME/KEY: CDS
      :   LOCATION: 3..884
      :
      : SEQUENCE DESCRIPTION: SEQ ID NO: 10:
      :
      : US-09-215-649A-10

```

Query Match	8.4%;	Score 97;	DB 4;	Length 1630;
Best Local Similarity	67.2%;	Pred. No. 8e-22;		
Matches 170;	Conservative	0;	Mismatches 75;	Indels 8;
				Gaps 2

```
?      SEQUENCE CHARACTERISTICS:  
?          LENGTH: 1630 base pair  
?          TYPE: nucleic acid  
?          STRANDEDNESS: single  
?          TOPOLOGY: linear  
?          MOLECULE TYPE: cDNA  
?          HYPOTHEetical: NO  
?          ANTI-SENSE: NO  
?          ORIGINAL SOURCE:  
?              ORGANISM: Mus musculus  
?          IMMEDIATE SOURCE:
```

```

1      RESULT 10
2      US-08-989-362-1
3      ; Sequence 1, Application US/08989362
4      ; Patent No. 6242586
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Gorman, Daniel M.
7      ; APPLICANT: Mattson, Jeanine D.
8      ; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
9      ; TITLE OF INVENTION: Reagents
10     ; NUMBER OF SEQUENCES: 2
11     ; CORRESPONDENCE ADDRESSES:
12     ; ADDRESSEE: DMAX Research Institute
13     ; STREET: 901 California Avenue
14     ; CITY: Palo Alto
15     ; STATE: California
16     ; COUNTRY: USA
17     ; ZIP: 94304-1104
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/989,362
25     ; FILING DATE: 12-Dec-1997
26     ; CLASSIFICATION: 56
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: US 60/032,846
29     ; FILING DATE: 13-Dec-1996
30     ; ATTORNEY/AGENT INFORMATION:
31     ; NAME: Ching, Edwin P.
32     ; REGISTRATION NUMBER: 34,090
33     ; REFERENCE/DOCKET NUMBER: DX0686
34     ; TELECOMMUNICATION INFORMATION:
35     ; TELEPHONE: (650)852-9196
36     ; TELEFAX: (650)496-1204
37     ; INFORMATION FOR SEQ ID NO: 1:
38     ; SEQUENCE CHARACTERISTICS:
39     ; LENGTH: 2191 base pairs
40     ; TYPE: nucleic acid
41     ;

```


	Query Match	4.6%	Score 53;	DB 1;	Length 7218;	
	Best Local Similarity	6.2%;	Pred.No. 8.4e-07;			
	Matches	26;	Conservative	220;	Mismatches 175;	Indels 0; Gaps 0
QY	116	GGATAGGAGGTGGTTCGAGACATGAGGAAGTTCTACAGAGGCGACACTGGG	175			
Db	1439	GGTACRRR	1380			
QY	176	CTTAGCAGCACCCCTGCCTTGAGAGGCGTGTGAGAGTGGGAAATAATCCGACTGCC	235			
Db	1379	RR	1320			
QY	236	TCTCTTCATCTCTCCCCAACCCACGAGGGTGTGTGGGCCCCACAGCGAGCCTCCC	295			
Db	1319	RR	1260			
QY	296	GGGAGAGAAGTGAGAGAGACCTGGAGGGCCGATAGAAGTAAGCACACAAGTACTA	355			
Db	1259	RR	1200			
QY	356	CAGGCAACGAGCATTTTTTGAGCATTTGGATTGTGACAAACAATCGACAAAAA	415			
Db	1199	RR	1140			

[illegible]

RESULT 15
US-09-244-796-17
; Sequence 17, Application US/09244796
; Patent No. 6261344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.


```
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ. ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match      3.28; Score 37; DB 4; Length 289;
Best Local Similarity 4.6%; Pred. No. 0.021;
Matches 10; Conservative 98; Mismatches 109; Indels 0; Gaps 0;

QY 829 AGAGCCTAGAAGAGGGCCAGCAGGTGCTGCTCACTTGAGCCCGGAGAGCAGGAG 888
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 1  KRGGRARARARURURARURURARURURARARARURURARARURURGRNRN 60
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
QY 889 TGGGTGCTGGGCTGAGAACCAAGTATGCGCCCTGGGAGCGCCGGAGAGATGAGT 948
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 61 RSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRN 120
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
QY 949 TTTGAGGCAAGGATTTGCATTGTGATGACTGTGTGTGCTGAGGCTGAGAGT 1008
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 121 RSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRN 180
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
QY 1009 TGTACTCTGAACACAGACAAAGCATGATGTGATG 1045
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 181 RSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRN 217
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
```

Search completed: December 8, 2002, 17:28:19
Job time : 91.8321 secs

•
•
•
•

Tue Dec 10 10:51:37 2002

us-09-880-457-1_copy_543_746.nri

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:19 ; Search time 11.9188 Seconds
(without alignments)
5249.015 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204
Sequence: 1 catgagcctcataaagag.....gtatttgagatcattcac 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	96.4	47.3	954 3 US-08-996-139-12	Sequence 12, Appl
2	96.4	47.3	954 4 US-08-995-659-12	Sequence 12, Appl
3	96.4	47.3	954 4 US-09-215-649A-12	Sequence 12, Appl
4	96.4	47.3	954 4 US-09-577-780-12	Sequence 12, Appl
5	96.4	47.3	2271 4 US-09-052-521C-3	Sequence 3, Appl1
6	80.8	39.6	1630 3 US-08-996-139-10	Sequence 10, Appl
7	80.8	39.6	1630 4 US-08-995-659-10	Sequence 10, Appl
8	80.8	39.6	1630 4 US-09-215-649A-10	Sequence 10, Appl
9	80.8	39.6	2191 4 US-08-989-362-1	Sequence 1, Appl1
10	80.8	39.6	2295 2 US-08-842-842-6	Sequence 6, Appl1
11	80.8	39.6	2295 2 US-09-052-521C-1	Sequence 1, Appl1
12	80.8	39.6	2295 2 US-07-968-971A-5	Sequence 5, Appl1
13	29.4	14.4	1461 1 US-07-824-247-47	Sequence 47, Appl
14	29.4	14.4	1461 1 US-08-142-473A-7	Sequence 7, Appl1
15	29.4	14.4	1461 1 US-08-464-523B-9	Sequence 9, Appl1
16	29.4	14.4	1461 1 US-08-469-203A-7	Sequence 7, Appl1
17	29.4	14.4	1461 1 US-08-469-203A-7	Sequence 7, Appl1
18	29.4	14.4	1461 1 US-08-470-204A-47	Sequence 47, Appl
19	29.4	14.4	1461 3 US-08-926-522-12	Sequence 12, Appl
20	29.4	14.4	1461 2 US-08-768-964-14	Sequence 14, Appl
21	28.4	13.9	522 2 US-08-768-964-15	Sequence 15, Appl
22	28.4	13.9	522 2 US-09-005-299-14	Sequence 14, Appl
23	28.4	13.9	522 3 US-09-005-299-15	Sequence 15, Appl
24	28.4	13.9	522 3 US-09-515-431-14	Sequence 14, Appl
25	28.4	13.9	522 4 US-09-515-431-15	Sequence 15, Appl
26	28.4	13.9	522 4 US-08-768-964-11	Sequence 11, Appl
27	28.4	13.9	597 2 US-08-768-964-11	Sequence 11, Appl

C 28	28.4	13.9	597 2 US-08-768-964-16	Sequence 16, Appl
C 29	28.4	13.9	597 3 US-09-005-299-11	Sequence 11, Appl
C 30	28.4	13.9	597 3 US-09-005-299-16	Sequence 16, Appl
C 31	28.4	13.9	597 4 US-09-515-431-11	Sequence 11, Appl
C 32	28.4	13.9	597 4 US-09-515-431-16	Sequence 16, Appl
C 33	28.4	13.9	714 2 US-08-768-964-6	Sequence 6, Appl1
C 34	28.4	13.9	714 3 US-09-005-299-6	Sequence 6, Appl1
C 35	28.4	13.9	714 3 US-09-005-299-8	Sequence 8, Appl1
C 36	28.4	13.9	714 4 US-09-515-431-6	Sequence 6, Appl1
C 37	28.4	13.9	714 4 US-09-515-431-8	Sequence 4, Appl1
C 38	28.4	13.9	789 2 US-08-768-964-4	Sequence 4, Appl1
C 39	28.4	13.9	789 2 US-08-768-964-5	Sequence 5, Appl1
C 40	28.4	13.9	789 3 US-09-005-299-4	Sequence 4, Appl1
C 41	28.4	13.9	789 3 US-09-005-299-5	Sequence 5, Appl1
C 42	28.4	13.9	789 4 US-09-515-431-4	Sequence 4, Appl1
C 43	28.4	13.9	789 4 US-09-515-431-5	Sequence 5, Appl1
C 44	28.4	13.9	789 2 US-08-768-964-1	Sequence 1, Appl1
C 45	28.4	13.9	1069 2 US-08-768-964-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-996-139-12

Query Match
Best Local Similarity 47.3%; Score 96.4; DB 3; Length 954;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATTAACGAGCTTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTC 62
Db 531 TGGTCCCAATAAGTAGCTGCTCTCTGTCATGATGGGTTGGCCCAAGATCTC 116
QY 63 CAACATGACTTTGACGAGCAAGAACTAAGATCA-----AAGCATTATTACCGGAA 116
Db 591 CAACATGACTTTGACGAGCAAGAACTAAGATCAAGATGCTTTATTACTCTGA 650
QY 117 TGCCGACATTTGCTCGACATGCGCTAAGCTCAGCAGGCTTAAGTCTGACGACCTTCA 176
Db 651 TGGCAACATTTGCTTGCACATCATGAACCTCAGAGAGCTTACGAGTACTTCTCA 710
QY 177 GCTA 180
Db 711 ACTA 714

RESULT 2

US-08-995-659-12
Sequence 12, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Marskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 7.5.5
CURRENT APPLICATION DATA:
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-995-659-12

Query Match
Best Local Similarity 47.3%; Score 96.4; DB 4; Length 954;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATTAACGAGCTTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTC 62
Db 531 TGGTCCCAATAAGTAGCTGCTCTCTGTCATGATGGGTTGGCCCAAGATCTC 116
QY 63 CAACATGACTTTGACGAGCAAGAACTAAGATCA-----AAGCATTATTACCGGAA 116
Db 591 CAACATGACTTTGACGAGCAAGAACTAAGATCAAGATGCTTTATTACTCTGA 650
QY 117 TGCCGACATTTGCTCGACATGCGCTAAGCTCAGCAGGCTTAAGTCTGACGACCTTCA 176
Db 651 TGGCAACATTTGCTTGCACATCATGAACCTCAGAGAGCTTACGAGTACTTCTCA 710
QY 177 GCTA 180
Db 711 ACTA 714

RESULT 3

US-09-215-649A-12
Sequence 12, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Marskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 7.5.5
CURRENT APPLICATION DATA:
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>

```

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hurankl (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-215-649A-12

```

```

Query Match          47.3%; Score 96.4; DB 4; Length 954;
Best Local Similarity 74.5%; Pred. No. 5.7e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1

QY      3  TGAGGCTCAATAAACGAGTCTTCTCTCTGGAACATGACCAAGATTGGGCAACGCTCTC 62
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      531  TGGTTCCTCAATAACTGAGTCTGTCCCTTCGTGATACCATGATCGGGGTGGGCAAGATCTC 590
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      63  CAACATGACTCTTGACGACCGAAACACTAAGATCA-----AAGCATTTATTACCGGAA 116
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      591  CAACATGACTTTTGGCAATGAAACACTAATAGTTATCATCGAGATGGCTTTTATTAACCTCTA 650
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      117  TGGCCAGATTTGGCTGCTGACATGCGCTTAACCTGACGAGGCGCTTACTCTGACAGACCTCTCA 176
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      651  TCCCAACACTTTTGCTTCTTCGACATCATGAAACTTCAGAGAGACCTTAAGACAGAGTATCTTCA 710
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      177  GCTA 180
      11  | | |
Db      711  ACTA 714

RESULT 4
US-09-577-780-12
; Sequence 12, Application US/09577780
; Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
              Galibert, Laurent
              Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

```

```

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Parkirs, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)213-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hurankl (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-577-780-12

```

```

Query Match          47.3%; Score 96.4; DB 4; Length 954;
Best local Similarity 74.5%; Freq. No. 3 7e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1.

QY      3 TGAGGCTCATAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATGGGCAACGCTC 62
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      531 TGTGTCCTCAATAAGTGATGTCTGTCTTCTTGTACCATATGCGGGTGGCCAGATCTC 590
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      63 CACATGACTTTGAGCAACGAAACTAGACTCA-----AAGGCATTATTTACGGAA 116
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      591 CACATGACTTTAGCAATGGAAACTAATAGTTATTCAGATGGCTTTTATTTACCTGTA 650
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      117 TGCCGACATTTGCTCTCTGACATGGCGTAACCCGAGGCGCTAACTCTGCAGGACCTTCA 176
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      651 TGCCACCATTTGCTTGTGACATCATGTAACTTAGAGAGACACTAGCTACAGAGATCTTCA 710
      11 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      177 GCTA 180
      11 | | |
DB      711 ACTA 714

RESULT 5
US-09-052-521C-3
; Sequence 3, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Bv
CURRENT APPLICATION NUMBER: US/09/052.521C
CURRENT FILING DATE: 1998-03-30
PRIORITY APPLICATION NUMBER: 08/880,855
PRIORITY FILING DATE: 1997-06-23
PRIORITY APPLICATION NUMBER: 08/842,842

```

;; PRIOR FILING DATE: 1997-04-16
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 2271
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (185)..(1135)
US-09-052-521C-3

Query Match 47.3%; Score 96.4; DB 4; Length 2271;
Best Local Similarity 74.5%; Pred. No. 5.9e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAACGAGCTTCTCTCTGGAACATGACCAAGATTGGGCAACGCTC 62
DB 715 TCGTCCCATTAAGTAGTGTCTCTGTTGATGATCGGGGTGGCCCAAGATCTC 774
QY 63 CAACATGACTTTCAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGGA 116
DB 775 CAACATGACTTTCAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGGA 116
QY 117 TGGCAGATTGCTCTGACATCGGTAACCTCAGCAGCCTTAAGCTGACGAGCTTCA 834
DB 835 TGGCAACATTGCTCTGACATCATGAAACTTCAGGAGACCTACTACAGAGTATCTTCA 894
QY 177 GCTA 180
DB 895 ACTA 898

RESULT 6
US-08-996-139-10

;; Sequence 10, Application US/08996139
;; Patent No. 6017729
;; GENERAL INFORMATION:

;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/996,139
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1630 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mus musculus
;; IMMEDIATE SOURCE:
;; LIBRARY:

;; CLONE: RANKL
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..884
US-08-996-139-10

Query Match 39.6%; Score 80.8; DB 3; Length 1630;
Best Local Similarity 70.2%; Pred. No. 3.2e-20;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 8 CTCATTAACGAGCTTCTCTCTTGGAAACATGACCAAGATTGGGCAACGCTCCACA 67
DB 469 CCCATTAAGTCACTCTGCTCTGTTGATGATCGGGGTGGCCCAAGATCTTACA 528
QY 68 TGACTTTCAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGGAATGCCG 121
DB 529 TGACGTTAAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGGAATGCCG 121
QY 122 ACATTGCTCTGACATCGGTAACCTCAGCAGCCTTAAGCTGACGAGCTTCA 179
DB 589 ACATTGCTCTGACATCATGAAACTTCAGGAGACCTACTACAGACTTCTTCA 646

RESULT 7
US-08-995-659-10

;; Sequence 10, Application US/08995659
;; Patent No. 624213
;; GENERAL INFORMATION:

;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/995,659
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:

```

1      APPLICATION NUMBER: 08/996,139
2      FILING DATE: <Unknown>
3      APPLICATION NUMBER: USSN 08/813,509
4      FILING DATE: 07 MARCH 1997
5      APPLICATION NUMBER: USSN 08/772,330
6      FILING DATE: 23 DECEMBER 1996
7
8      ATTORNEY/AGENT INFORMATION:
9      NAME: Perkins, Patricia Anne
10     REGISTRATION NUMBER: 34,693
11     REFERENCE/DOCKET NUMBER: 2851-A
12
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: (206)587-0430
15     TELEFAX: (206)233-0644
16
17     INFORMATION FOR SEQ ID NO: 10:
18
19     SEQUENCE CHARACTERISTICS:
20
21     LENGTH: 1630 base pairs
22     TYPE: nucleic acid
23     STRANDEDNESS: single
24     TOPOLOGY: linear
25     MOLECULE TYPE: cDNA
26     HYPOTHETICAL: NO
27     ANTI-SENSE: NO
28     ORIGINAL SOURCE:
29     ORGANISM: Mus musculus
30
31     IMMEDIATE SOURCE:
32     CLONE: RANKL
33     LIBRARY: <Unknown>
34
35     FEATURE:
36     NAME/KEY: CDS
37     LOCATION: 3..884
38     SEQUENCE DESCRIPTION: SEQ ID NO: 10:
39
40     US-09-215-669A-10

```

```

Query Match Similarity      39.6%;      Score 80.8;  DB 4;      Length 1930,
Best Local 15;      Cons: 0;      Pred. No. 3,2e-20;
Matches 125;      Conservative 0;      Mismatches 47;      Indels 6;      Gaps 1

      QY      8      CTCATATAACAGAGTCTTCTTCTTGGAAACATATACCAAGATTGGGCAACGCTCTCCACA      67
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
      Db      469      CCCATTAAAGTCACTCTGCTCTCTGGTACCAAGATCGAGCTGGGCCAAGATCTCTACCA      528
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
      QY      68      TGACCTTCGACGACGAAACATAAGATCA-----AAGCATTTATTACGGAAATGCG      121
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
      Db      529      TGACGTTAGCAACGAAACATAAGGTTAACCAAGATGGCTCTATTACCTGTGCGCA      588
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
      QY      122      ACATTTGCTCTCGACATCGCGTAACCTCAGACGCCCTTAACCTGCGAGACCTTCAGCT      179
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
      Db      589      ACATTTGCTCTGGCATCATGAAACATCGGGGAAGCGTACTACAGACTATCTTCAGCT      646
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |

RESULT 9
US-09-577-780-10
: Sequence 10, Application US/095777780
: Patent No. 6419929
:
: GENERAL INFORMATION:
:
: APPLICANT: Anderson, Dirk M.
: Galibert, Laurent
: Maraskovsky, Eugene
:
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
:
: NUMBER OF SEQUENCES: 19
:
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
:
: STATE: WA
:
: COUNTRY: USA
:
: ZIP: 98101
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: Apple Power Macintosh
:
: OPERATING SYSTEM: Apple Operating System 7.5.5
:
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
:
: CURRENT APPLICATION DATA:

```


APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-577-780-10

Query Match
Best Local Similarity 39.6%; Score 80.8; DB 4; Length 1630;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

DB 8 CTCATAAAGAGCTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTCCACA 67
469 CCCATAAGTCACTCTCTCTTGTGACGATGAGGCTGGGCCAAGATCTTAACA 528
QY 68 TGACTTTCACCAAGGAAACATAAGATCA-----AAGCATTTATTAACCGGAATGCCG 121
DB 529 TGAAGTTAAGCAAGGAAACATAAGGTTAACCAAGATGCTTCTATTACTGTAGCCCA 588
QY 122 ACATTGCTCTCGACATCGGTAACTCAGACAGGCTTAACCTTGACGAGCTTCAAGCT 179
DB 589 ACATTGCTCTCGACATCGGTAACTCAGACAGGCTTAACCTTGACGAGCTTCAAGCT 646

RESULT 10
US-08-989-362-1
Sequence 1, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)496-1204
TELEFAX: (650)852-9196
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 125..1072
US-08-989-362-1

Query Match
Best Local Similarity 39.6%; Score 80.8; DB 4; Length 2191;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

DB 8 CTCATAAAGAGCTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTCCACA 67
DB 657 CCCATAAGTCACTCTCTCTTGTGACGATGAGGCTGGGCCAAGATCTTAACA 716
QY 68 TGACTTTCACCAAGGAAACATAAGATCA-----AAGCATTTATTAACCGGAATGCCG 121
DB 717 TGAAGTTAAGCAAGGAAACATAAGGTTAACCAAGATGCTTCTATTACTGTAGCCCA 776
QY 122 ACATTGCTCTCGACATCGGTAACTCAGACAGGCTTAACCTTGACGAGCTTCAAGCT 179
DB 777 ACATTGCTCTCGACATCGGTAACTCAGACAGGCTTAACCTTGACGAGCTTCAAGCT 834

RESULT 11
US-08-842-842-6
Sequence 6, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOCALCIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451

US-07-824-247-47
; Sequence 47, Application US/07824247

Patent No. 5512482
GENERAL INFORMATION:
APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/824,247
FILING DATE: 19920122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
FILING DATE: 24-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
FILING DATE: 7-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/704,861
FILING DATE: 21-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02960
FILING DATE: 25-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,007
FILING DATE: 27-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,426
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/514,030
FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 82-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: PCR product from mRNA template
US-07-824-247-47
Query Match 14.4%; Score 29.4; DB 1; Length 1461;
Best Local Similarity 56.8%; Pred. No. 0.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 10 CATAAAGAGCTCTTCTCTTGGAAACATGACCAAGATTGGGCAAAAGCTTCCACATG 69
DB 1241 CAGAAATCAGGCTGCTGTTTAGATATATATCCAAAAATGTCCTATATGTCAGAAACTT 1300
QY 70 ACTTTGACGACGGAAGAACTAAGAGTCAAGGCAT 104
DB 1301 AATATCAGAAAATAATCAATGATGATCAAGTTAT 1335

RESULT 15
US-08-142-473A-7
Sequence 7, Application US/08142473A
Patent No. 5639790
GENERAL INFORMATION:
APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
COMPUTER: Apple Macintosh IIfx
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,473A
FILING DATE: 18-NOV-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04332
FILING DATE: 21-MAY-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/824,247
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
FILING DATE: 24-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
FILING DATE: 7-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/704,861
FILING DATE: 21-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 82-4 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-08-142-473A-7
Query Match 14.4%; Score 29.4; DB 1; Length 1461;
Best Local Similarity 56.8%; Pred. No. 0.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 10 CATAAAGAGCTCTTCTCTTGGAAACATGACCAAGATTGGGCAAAAGCTTCCACATG 69
DB 1241 CAGAAATCAGGCTGCTGTTTAGATATATATCCAAAAATGTCCTATATGTCAGAAACTT 1300
QY 70 ACTTTGACGACGGAAGAACTAAGAGTCAAGGCAT 104
DB 1301 AATATCAGAAAATAATCAATGATGATCAAGTTAT 1335

Tue Dec 10 10:51:37 2002

Search completed: December 8, 2002, 17:28:32
Job time : 17.918 secs

us-09-880-457-1_copy_543_746.rni

111

Tue Dec 10 10:51:46 2002

US-09-880-457-4_COPY_20_87.rapb

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 8, 2002, 19:31:38 ; Search time 10.0903 Seconds
(without alignments)
109,459 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAKTSLSSWKHDQMANV.....TSAGTLDPDQLQMCNLRITH 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PublishedApplications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCOT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/PCMS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCMS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	373	100.0	87	10 US-09-880-457-4	Sequence 4, App1
2	358	96.0	94	10 US-09-880-457-5	Sequence 5, App1
3	358	96.0	95	10 US-09-880-457-6	Sequence 6, App1
4	178	47.7	160	9 US-09-779-050A-15	Sequence 15, App1
5	178	47.7	317	9 US-09-877-650-13	Sequence 13, App1
6	178	47.7	317	10 US-09-871-856-13	Sequence 13, App1
7	178	47.7	317	10 US-09-871-856-13	Sequence 2, App1
8	174	46.6	245	9 US-10-017-910-2	Sequence 14, App1
9	172	46.1	160	9 US-09-779-050A-14	Sequence 11, App1
10	172	46.1	294	9 US-09-871-856-11	Sequence 11, App1
11	172	46.1	316	9 US-10-017-910-4	Sequence 8, App1
12	112.5	30.2	109	10 US-09-911-777-8	Sequence 5085, Ap
13	112.5	30.2	813	10 US-09-815-242-5085	Sequence 5, App1
14	63.5	17.0	813	10 US-09-924-841-5	Sequence 9, App1
15	59.5	16.0	329	10 US-09-924-841-9	Sequence 334, App
16	59.5	15.0	484	10 US-09-801-368-334	Sequence 1, App1
17	56	14.9	679	12 US-10-119-714-1	Sequence 760, App
18	55.5	14.9	753	10 US-09-925-302-760	
19	55.5	14.9	753	10 US-09-925-302-760	

20	55	14.7	57	10 US-09-864-761-42649	Sequence 42649, A
21	54.5	14.6	333	10 US-09-924-841-10	Sequence 10, App1
22	54	14.5	146	9 US-09-779-050A-10	Sequence 16, App1
23	54	14.5	149	10 US-09-934-465-16	Sequence 2, App1
24	54	14.5	261	10 US-09-842-745A-2	Sequence 10, App1
25	54	14.5	323	10 US-09-280-197-10	Sequence 2, App1
26	54	14.5	1091	9 US-09-423-126-2	Sequence 39850, A
27	54	14.5	1091	10 US-09-280-197-2	Sequence 4, App1
28	53	14.2	77	10 US-09-864-761-39850	Sequence 4, App1
29	53	14.2	204	10 US-09-866-582-4	Sequence 4, App1
30	53	14.2	220	9 US-10-133-178-4	Sequence 4, App1
31	53	14.2	764	10 US-09-747-521-4	Sequence 4, App1
32	53	14.2	764	10 US-10-106-014-4	Sequence 4, App1
33	53	14.2	1136	10 US-09-815-242-12447	Sequence 12447, A
34	53	14.2	1136	10 US-09-815-242-12814	Sequence 12814, A
35	53	14.2	1179	9 US-09-815-242-5522	Sequence 5522, Ap
36	52.5	14.1	577	9 US-10-047-542-66	Sequence 66, App1
37	52	13.9	261	10 US-09-245-764-7	Sequence 7, App1
38	52	13.9	294	9 US-10-027-806-12	Sequence 12, App1
39	52	13.9	593	10 US-09-943-446-9	Sequence 9, App1
40	52	13.9	595	10 US-09-943-446-6	Sequence 6, App1
41	52	13.9	953	10 US-09-354-453-36	Sequence 36, App1
42	51.5	13.8	972	10 US-09-924-154-16	Sequence 16, App1
43	51	13.7	318	12 US-10-032-626-2	Sequence 2, App1
44	51	13.7	394	9 US-09-992-598-422	Sequence 422, App
45	51	13.7	394	9 US-09-989-293A-422	Sequence 422, App

ALIGNMENTS

RESULT 1
US-09-880-457-4 Application US/09880457
Sequence 4, App1
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-4

Query Match	100.0%	Score 373;	DB 10;	Length 87;
Best Local Similarity	100.0%	Pred. No. 7.3e-41;		
Matches	68;	Conservative	0;	Mismatches
Db	20	HEAKTSLSSWKHDQMANVSMTEFSGKLRKGYRRNADICSRHVTSGAGTLDPDL	79	
Qy	1	HEAKTSLSSWKHDQMANVSMTEFSGKLRKGYRRNADICSRHVTSGAGTLDPDL	60	
Db	61	WCNLRITH 68		
Qy	80	WCNLRITH 87		
Db	80	WCNLRITH 87		
RESULT 2	US-09-880-457-5	Application US/09880457		
Sequence 5, App1	Patent No. US20020106728A1			
GENERAL INFORMATION:				
APPLICANT: Pan, James				
APPLICANT: Goddard, Audrey				

```

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 5
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-457-5
```

```
Query Match
Best Local Similarity 96.0%; Score 358; DB 10; Length 94;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 HEAHTSLSSMKHDDMANVSNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 60
DB 20 HEAHTSLSSMKHDDMANVSNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 60
OY 61 WCNLRIT 67
DB 80 WCNLRSV 86
```

```

RESULT 3
US-09-880-457-6
; Sequence 6, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 6
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-457-6
```

```
Query Match
Best Local Similarity 96.0%; Score 358; DB 10; Length 95;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 HEAHTSLSSMKHDDMANVSNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 60
DB 20 HEAHTSLSSMKHDDMANVSNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 60
OY 61 WCNLRIT 67
DB 80 WCNLRSV 86
```

```

RESULT 4
US-09-779-050A-15
; Sequence 13, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
```

```

; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-15
```

```
Query Match
Best Local Similarity 47.7%; Score 178; DB 9; Length 160;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
```

```
OY 3 AHKTSLSMKHDDMANVSNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 60
DB 22 SHKVSLSWHDGMAKISNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 81
```

```

RESULT 5
US-09-877-650-13
; Sequence 13, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maizkovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13
```

```
Query Match
Best Local Similarity 47.7%; Score 178; DB 9; Length 317;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
```


; APOTECH S.A.
 ; BROWNING, Jeffrey
 ; APPLICANT:
 ; AMBROSE, Christine
 ; APPLICANT:
 ; MACKAY, Fabienne
 ;

ORGANISM: Pseu
US-09-815-242-5085

Query Match	17.0%	Score 63.5:	DB 10:	Length 813:
Best Local Similarity	28.8%	Pred. No. 3.5:		
Matches 19, Conservative	11, Mismatches	23:	Indels 13:	Gaps 3

OY 6 TSLSSWKHDQDANVSNMTEFSGK-LRVKGI-----YRNADICSRHRYT---SAG 52
DB 711 TAYLOYKRPDADNNNRQATFFFSKDYRLDGVSESGRRQVSTYTYVDLVASQYRITPDQLS 770
OY 53 LTLQDL 58
DB 771 LGIQNL 776

RESULT 15

US-09-924-841-5
; Sequence 5, Application US/09924841
; Patent No. US20020127633A1
; GENERAL INFORMATION:
; APPLICANT: Dilley, David R
; APPLICANT: Kadyrzhanova, Dina K
; APPLICANT: Warner, Toni M
; TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
; FILE REFERENCE: MS041-453
; CURRENT APPLICATION NUMBER: US/09/924,841
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/413,231
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 329
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
; NAME/KEY: MUTAGEN
; LOCATION: (210)
; OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-5

Query Match 16.0%; Score 59.5; DB 10; Length 329;
Best Local Similarity 25.7%; Pred. No. 3.7;
Matches 18; Conservative 10; Mismatches 33; Indels 9; Gaps 2;
OY 1 HEAHTSLSMKHD-----QDMANVSNMTEFSGK-LRVKGIYRNADICSRHRYTSA 51
DB 60 NEFGAMTQDEKHDLAHAYNPDPNPHVNGYKAVGKRAVESFCYLNPDGEGDHPMIAA 119
OY 52 GLTLQDLQIW 61
DB 120 GTPMHEVNIW 129

Search completed: December 8, 2002, 19:36:16
Job time: 11.0903 secs

Tue Dec 10 10:51:41 2002

us-09-880-457-4.iabp

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 19:31:38 ; Search time 12.9097 Seconds
(without alignments)
109.459 Million cell updates/sec

Title: US-09-880-457-4

Perfect score: 455
Sequence: 1 MATLITSLQILLIPISHS.....TSAGTLQDLOLQNCNLRITIH 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications-AA:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	455	100.0	87	10	US-09-880-457-4
2	440	96.7	95	10	US-09-880-457-6
3	434	95.4	94	10	US-09-880-457-5
4	180.5	39.7	160	9	US-09-779-050A-15
5	180.5	39.7	317	9	US-09-877-650-13
6	180.5	39.7	317	10	US-09-813-856-13
7	180.5	39.7	317	10	US-09-871-856-13
8	176.5	38.8	245	9	US-10-017-910-2
9	176.5	38.7	294	9	US-09-877-650-11
10	176.5	38.7	294	9	US-09-871-856-11
11	176.5	38.7	316	9	US-10-017-910-4
12	176.5	38.7	316	9	US-09-911-777-8
13	115	25.3	109	10	US-09-815-242-5085
14	63.5	14.0	329	10	US-09-924-841-5
15	61.5	13.5	329	10	US-09-924-841-9
16	61.5	13.5	528	10	US-09-792-200B-22
17	61	13.4	716	10	US-09-853-533A-2
18	60	13.0	220	9	US-10-133-178-4
19	59				

20	57	12.5	441	10	US-09-815-242-4986	Sequence 4986, Ap
21	57	12.5	720	10	US-09-801-368-176	Sequence 176, Ap
22	56.5	12.4	333	10	US-09-924-841-10	Sequence 10, Appl
23	56.5	12.4	753	10	US-09-925-302-760	Sequence 760, Appl
24	56	12.3	484	10	US-09-801-368-334	Sequence 334, Ap
25	56	12.3	529	10	US-09-925-301-866	Sequence 866, Appl
26	56	12.3	878	12	US-10-060-332-2	Sequence 2, Appl
27	55.5	12.2	146	9	US-09-779-050A-10	Sequence 10, Appl
28	55.5	12.2	149	10	US-09-842-465-16	Sequence 16, Appl
29	55.5	12.2	261	10	US-09-842-745A-2	Sequence 2, Appl
30	55.5	12.2	679	12	US-10-119-714-1	Sequence 1, Appl
31	55	12.1	57	10	US-09-864-761-42649	Sequence 42649, A
32	55	12.1	821	9	US-09-764-868-883	Sequence 883, Ap
33	55	12.1	1151	10	US-09-801-368-266	Sequence 266, Ap
34	54.5	12.0	579	10	US-09-824-558-2	Sequence 2, Appl
35	54.5	12.0	771	10	US-09-801-368-326	Sequence 326, Ap
36	54	11.9	143	9	US-09-779-050A-19	Sequence 19, Appl
37	54	11.9	192	9	US-09-764-868-1192	Sequence 1192, Ap
38	54	11.9	239	10	US-09-921-667-4	Sequence 4, Appl
39	54	11.9	323	10	US-09-280-197-10	Sequence 10, Appl
40	54	11.9	1091	9	US-09-423-126-2	Sequence 2, Appl
41	54	11.9	1091	10	US-09-280-197-2	Sequence 12447, A
42	54	11.9	1136	10	US-09-815-242-12447	Sequence 12814, A
43	54	11.9	1136	10	US-09-815-242-12814	Sequence 5522, Ap
44	54	11.9	1179	10	US-09-815-242-5522	Sequence 13, Appl
45	53.5	11.8	246	10	US-09-855-544A-13	

ALIGNMENTS

RESULT 1
US-09-880-457-4
Sequence 4, Application US/09880457
Patient No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: For the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-4

Query Match 100.0%; Score 455; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATLITSLQILLIPISHSHEAKTSLSSKRDQWAVSNMTSNGKLRVKGITYRNAD 60
Db 1 MATLITSLQILLIPISHSHEAKTSLSSKRDQWAVSNMTSNGKLRVKGITYRNAD 60
QY 61 ICSHRVTSAGTLQDLOLQNCNLRITIH 87
Db 61 ICSHRVTSAGTLQDLOLQNCNLRITIH 87

RESULT 2
US-09-880-457-6
Sequence 6, Application US/09880457
Patient No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey

APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 6
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-6

Query Match
Best Local Similarity 96.7%; Score 440; DB 10; Length 95;
Matches 84; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAILTSLQILLIPISHEAKRTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
DB 1 MAILTSLQILLIPISHEAKRTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
QY 61 ICSRHRVTSAGLTLDLQMLCNLRV 86
DB 61 ICSRHRVTSAGLTLDLQMLCNLRV 86

RESULT 3
US-09-880-457-5
Sequence 5, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-5

Query Match
Best Local Similarity 95.4%; Score 434; DB 10; Length 94;
Matches 83; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAILTSLQILLIPISHEAKRTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
DB 1 MAILTSLQILLIPISHEAKRTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
QY 61 ICSRHRVTSAGLTLDLQMLCNLRV 86
DB 61 ICSRHRVTSAGLTLDLQMLCNLRV 86

RESULT 4
US-09-779-050A-15
Sequence 15, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A

CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-050A-15

Query Match
Best Local Similarity 39.7%; Score 180.5; DB 9; Length 160;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKRTSLSSWKHDQDANVSNMTFSGKLRV--GIYRNADICSRHRVTSAGL 72
DB 18 IPSGS---HKVSLSSWYHGRGAKISNMTFSGKLRVAGIYRNADICSRHRVTSAGL 72
QY 73 TLQDQL 79
DB 75 ATBYQL 81

RESULT 5
US-09-877-650-13
Sequence 13, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

Query Match 39.7%; Score 180.5; DB 9; Length 317;
Best Local Similarity 59.7%; Pred. No. 7e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAHTSLSSWKHDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGL 72
||| | ||||| ||: ||||| ||| | ||: ||| || |
DB 175 IPSGS---HKVSLSSWYHDKGMAKISMNMTFSNGKLIYNQDGFYLVANICFRHHETSGL 231

QY 73 TLQDLQL 79
: |||
DB 232 ATXYLQL 238

RESULT 6
US-09-813-329-7
; Sequence 7, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
; FILE REFERENCE: D0016.0p
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match 39.7%; Score 180.5; DB 10; Length 317;
Best Local Similarity 59.7%; Pred. No. 7e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAHTSLSSWKHDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGL 72
||| | ||||| ||: ||||| ||| | ||: ||| || |
DB 175 IPSGS---HKVSLSSWYHDKGMAKISMNMTFSNGKLIYNQDGFYLVANICFRHHETSGL 231

QY 73 TLQDLQL 79
: |||
DB 232 ATXYLQL 238

RESULT 7
US-09-871-856-13
; Sequence 13, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match 39.7%; Score 180.5; DB 10; Length 317;
Best Local Similarity 59.7%; Pred. No. 7e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAHTSLSSWKHDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGL 72
||| | ||||| ||: ||||| ||| | ||: ||| || |
DB 175 IPSGS---HKVSLSSWYHDKGMAKISMNMTFSNGKLIYNQDGFYLVANICFRHHETSGL 231

QY 73 TLQDLQL 79
: |||
DB 232 ATXYLQL 238

RESULT 8
US-10-017-910-2
; Sequence 2, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-871-856-11
Query Match 38.7%; Score 176; DB 10; Length 294;
Best Local Similarity 55.4%; Pred. No. 2.3e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
QY 17 SISHEAKTSLSSMKHDQMANVSNMTFSGKLRK--GIYYRNADICSRHRTSAGLT 74
DB 151 SIPSGSHKVTLSWYHDSGKAKISNMTLSNGKLRVNODGFYLYANICFRHHETSGSVPT 210
QY 75 ODLOL 79
DB 211 DYLOL 215
RESULT 12
US-10-017-910-4
Sequence 4, Application US/10017910
Patent No. US2002015970A1
GENERAL INFORMATION:
APPLICANT: Choi, Yongwon
Wong, Brian
Josien, Regis
Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-017-910-4
Query Match 38.7%; Score 176; DB 9; Length 316;
Best Local Similarity 55.4%; Pred. No. 2.5e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
QY 17 SISHEAKTSLSSMKHDQMANVSNMTFSGKLRK--GIYYRNADICSRHRTSAGLT 74
DB 173 SIPSGSHKVTLSWYHDSGKAKISNMTLSNGKLRVNODGFYLYANICFRHHETSGSVPT 232
QY 75 ODLOL 79
DB 233 DYLOL 237
RESULT 13
US-09-911-777-8
Sequence 8, Application US/09911777
Patent No. US20020037852A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: APOTEC S.A.
APPLICANT: BROMING, Jeffrey
APPLICANT: AMBROSE, Christine
APPLICANT: MACKAY, Fabienne
APPLICANT: TSCHOPE, Jurg
APPLICANT: SCHNEIDER, Pascal
TITLE OF INVENTION: BAF, Inhibitors thereof and their use
FILE REFERENCE: A070 US
CURRENT APPLICATION NUMBER: US/09/911,777
CURRENT FILING DATE: 2001-07-24
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo Sapien
US-09-911-777-8
Query Match 25.3%; Score 115; DB 10; Length 109;
Best Local Similarity 43.1%; Pred. No. 2.4e-07;
Matches 28; Conservative 4; Mismatches 15; Indels 18; Gaps 2;
QY 15 IPSISHEAKTSLSSMKHDQMANVSNMTFSGKLRKGIYYRNADICSRHRTSAGLT 74
DB 15 IPSGSHKVTLSWYHDSGKAKISNMTLSNGKLRVNODGFYLYANICFRHHETSGSDAT 56
QY 75 ODLOL 79
DB 57 DYLOL 61
RESULT 14
US-09-815-242-5085
Sequence 5085, Application US/09815242

```
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA-011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5085
LENGTH: 813
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5085

Query Match
Best Local Similarity 14.0%; Score 63.5; DB 10; Length 813;
Matches 19; Conservative 11; Mismatches 23; Indels 13; Gaps 3;

QY 25 TSLSMKHDODWANSNMTFSNGK-LRVKGT-----YYRNADICSRHVT---SAG 71
   : : | | | | : : | | : : | : : : | : : : | : : : |
Db 711 TAYLQYKPDADNNRLQATFDSKDYRLDGVSEFGRRQVSTYTVLDVSGYRITPDQLS 770
   : : | | : : | : : | : : | : : | : : | : : | : : | : : |

QY 72 LTLDL 77
   : : | : : |
Db 771 LGIONL 776

RESULT 15
US-09-924-841-5
Sequence 5, Application US/09924841
Patent No. US20020127633A1
GENERAL INFORMATION:
APPLICANT: Dilley, David R.
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
FILE REFERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/924,841
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/413,231
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 329
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
```

```
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
NAME/KEY: MUTAGEN
LOCATION: (210)
OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-5

Query Match
Best Local Similarity 13.5%; Score 61.5; DB 10; Length 329;
Matches 18; Conservative 12; Mismatches 36; Indels 9; Gaps 2;

QY 15 IPSISHEAHTSLSWKHD-----QDNANSNMTFS--NGRLRYKGIYYRNADICSRH 65
   : : | | | | : : | : : | : : | : : | : : | : : |
Db 55 LODVNEFHGAMTDQEKHDLAHAYPNDPNPHVNGYKAVPGKAVESFCYLNPFGEDH 114
   : : | : : | : : | : : | : : | : : | : : | : : | : : |

QY 66 RYTSAGLTLDDLDLW 80
   : : | : : | : : |
Db 115 PMIAAGTPMHEVNLW 129
```

Search completed: December 8, 2002, 19:36:15
Job time : 13.9097 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:18:27 ; Search time 11.9188 Seconds
(without alignments)
6674.007 Million cell updates/sec

Title: US-09-880-457-1_Copy_543_746

Perfect score: 204
Sequence: 1 catgagcctcataaagcag.....gtaattgagacatcac 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications -NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	1161	10	US-09-880-457-1
2	194	95.1	1186	10	US-09-880-457-3
3	194	95.1	2412	10	US-09-880-457-2
4	96.4	47.3	954	9	US-09-877-650-12
5	96.4	47.3	954	10	US-09-871-856-12
6	93.2	45.7	1823	9	US-10-017-910-1
7	80.8	39.6	1630	9	US-09-877-650-10
8	80.8	39.6	1630	10	US-09-871-856-10
9	80.8	39.6	2237	9	US-10-017-910-3
10	61	29.9	61	10	US-09-880-457-9
11	31.2	15.3	493	9	US-10-040-739-93
12	31.2	15.3	985	10	US-09-920-300A-1691
13	31.2	15.3	985	12	US-10-033-528-1691
14	31.2	15.3	3073	10	US-09-867-701-10910
15	31.2	15.3	3073	10	US-09-920-300A-1690
16	31.2	15.3	3073	12	US-10-033-528-1690
17	30	14.7	30	10	US-09-880-457-8
18	29.4	14.4	409	10	US-09-783-590-1953
19	29.4	14.4	454	10	US-09-864-761-14164

C	20	29.4	14.4	2244	10	US-09-764-864-153	Sequence 133, App
	21	28.6	14.0	1365	10	US-09-815-242-4243	Sequence 4243, Ap
	22	28.6	14.0	1365	10	US-09-815-242-8196	Sequence 8196, Ap
	23	28.2	13.8	477	10	US-09-759-143-92	Sequence 92, Appl
	24	28.2	13.8	477	10	US-09-780-669-92	Sequence 92, Appl
	25	28.2	13.8	477	10	US-09-030-606-92	Sequence 92, Appl
	26	28.2	13.8	477	10	US-09-822-827-92	Sequence 92, Appl
	27	28.2	13.8	477	10	US-09-115-453-92	Sequence 92, Appl
	28	28.2	13.8	2000	9	US-09-938-842A-4251	Sequence 4251, Ap
	29	27.8	13.6	666	10	US-09-764-864-590	Sequence 590, App
	30	27.8	13.6	2048	10	US-09-764-847-1468	Sequence 1468, Ap
	31	27.8	13.6	465237	10	US-09-933-267A-1	Sequence 1, Appli
	32	27.6	13.5	371	10	US-09-834-975-285	Sequence 285, App
	33	27.6	13.5	608	10	US-09-759-143-193	Sequence 193, App
	34	27.6	13.5	608	10	US-09-780-669-193	Sequence 193, App
	35	27.6	13.5	608	10	US-09-030-606-193	Sequence 193, App
	36	27.6	13.5	608	10	US-09-822-827-193	Sequence 193, App
	37	27.6	13.5	608	10	US-09-115-453-193	Sequence 193, App
	38	27.6	13.5	909	10	US-09-935-943-7	Sequence 7, Appli
	39	27.6	13.5	1873	10	US-09-834-975-756	Sequence 756, App
	40	27.6	13.5	1873	10	US-09-834-975-757	Sequence 757, App
	41	27.2	13.3	817	10	US-09-809-545A-7	Sequence 7, Appli
	42	27.2	13.3	2000	9	US-09-938-842A-4387	Sequence 4387, Ap
	43	27	13.2	27	10	US-09-880-457-7	Sequence 7, Appli
	44	27	13.2	280	10	US-09-294-093B-5098	Sequence 5098, Ap
	45	27	13.2	9542	10	US-09-764-847-1809	Sequence 1809, Ap

ALIGNMENTS

RESULT 1
US-09-880-457-1
Sequence 1, Application US/09880457
Patient No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
TITLE OF INVENTION: Wood, William I.
TITLE OF INVENTION: For the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-1

Query Match 100.0%; Score 204; DB 10; Length 1161;
Best Local Similarity 100.0%; Pred. No. 1.5e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CATGAGCCTCATAAACGAGCTCTTCTTGGAAACATGACCAATGGGCAACGTC	60
DB	543	CATGAGCCTCATAAACGAGCTCTTCTTGGAAACATGACCAATGGGCAACGTC	602
QY	61	TCCAACATGACTTTCAGCAACGGAACAACTAGAGTCAAGGCAATTAACCGGATGCG	120
DB	603	TCCAACATGACTTTCAGCAACGGAACAACTAGAGTCAAGGCAATTAACCGGATGCG	662
QY	121	GACATTTGCTCTGACACATCGCTAACCTCAGAGGCTTAATCGAGACCTTCAGCTA	180
DB	663	GACATTTGCTCTGACACATCGCTAACCTCAGAGGCTTAATCGAGACCTTCAGCTA	722
QY	181	TGCTGTAATTTGAGATCAATTCAC	204
DB	723	TGCTGTAATTTGAGATCAATTCAC	746

```

1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: 08/995,659
3      FILING DATE: 1997-12-22
4      APPLICATION NUMBER: USSN 08/813,509
5      FILING DATE: 07 MARCH 1997
6      APPLICATION NUMBER: USSN 08/772,350
7      FILING DATE: 23 DECEMBER 1996
8      ATTORNEY/AGENT INFORMATION:
9      NAME: Perkins, Patricia Anne
10     REGISTRATION NUMBER: 34,693
11     REFERENCE/DOCKET NUMBER: 2852-A
12     TELECOMMUNICATION INFORMATION:
13     TELEPHONE: (206)587-0430
14     TELEFAX: (206)233-0644
15     INFORMATION FOR SEQ ID NO: 12:
16     SEQUENCE CHARACTERISTICS:
17     LENGTH: 954 base pairs
18     TYPE: nucleic acid
19     STRANDEDNESS: single
20     TOPOLOGY: linear
21     MOLECULE TYPE: cDNA
22     HYPOTHETICAL: NO
23     ANTI-SENSE: NO
24     ORIGINAL SOURCE:
25     ORGANISM: Homo sapiens
26     IMMEDIATE SOURCE:
27     LIBRARY: <Unknown>
28     CLONE: huRAKRL (full length)
29     FEATURE:
30     NAME/KEY: CDS
31     LOCATION: 1..951
32     SEQUENCE DESCRIPTION: SEQ ID NO: 12:
33     US-09-877-650-12

```


TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-017-910-1

Query Match 45.7%; Score 93.2; DB 9; Length 1823;
Best Local Similarity 73.4%; Pred. No. 2,3e-22;
Matches 135; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGCATCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTCTC 62
DB 315 TGGTCCCATAAAGTACGTCTCTCTTGGTACCATGATCGGGGTGGGTAAGATCTC 374
QY 63 CAACATGACTTTCAGCAACGGAACCTAAGAGTCA-----AAGCATTTATTACCGGAA 116
DB 375 CACATGACTTTTAGCATGGAACAACTAATGTTAATCAGAGATGGCTTTATTACCTGTA 434
QY 117 TGGCAGACTTGTCTGAGATGCGCTAACCTCAGAGGCTTAACCTTGCAGAGACTTCA 176
DB 435 TGGCAACATTTGCTTTGACATCATGAACTCAGAGAGACTGATACAGATATCTTCA 494
QY 177 GCTA 180
DB 495 ACTA 498

RESULT 7

US-09-877-650-10
Sequence 10, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/913,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL
FEATURE:

NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-877-650-10

Query Match 39.6%; Score 80.8; DB 9; Length 1630;
Best Local Similarity 70.2%; Pred. No. 4e-18;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 8 CTCATTAACAGAGTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTCCACA 67
DB 469 CCCATTAAGTCACTCTGCTCTTCTTGTACACGATCGAGGCTGGCCAAAGATCTTACA 528
QY 68 TGACTTTCAGCAACGGAACCTAAGAGTCA-----AAGCATTTATTACCGGAATGCG 121
DB 529 TGACCTTAAGCAACGGAACCTAAGAGTCAAGATGAGCTTCTTATTACCTGACGCA 588
QY 122 ACATTGCTCTGACATGCGCTAACCTCAGCAGGCTTAACCTCTCAGAGACTTACGT 179
DB 589 ACATTGCTTTCGAGATCATGAACATCGGAGAGCTTACAGACTATCTTACGCT 646

RESULT 8

US-09-871-856-10
Sequence 10, Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne

```

RESULT 10
US-09-880-457-9
; Sequence 9, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: For the treatment of Body Weight Disorders
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 9
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning oligonucleotide
US-09-880-457-9

Query Match          29.9%; Score 61; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.5e-12;
Matches    61; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY      75 CAGCAACGGAAACTAAGAGTCGAAGGCATTATTACCGAATGCCGACATTGTGCTCG 134
         |||||||
db       1 CACACACGGAAACTAAGAGTCGAAGGCATTATTACCGAATGCCGACATTGTGCTCG 60

```



```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10910
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-867-701-10910

Query Match      15.3%; Score 31.2; DB 10; Length 3073;
Best Local Similarity 54.3%; Pred. No. 0.6; Mismatches 53; Indels 0; Gaps 0;
Matches 63; Conservative 0;

QY 11 ATAAAGGAGCTTTCTTGTGGAACATGACCAAGATTGGGCAACGCTCTCCACATGA 70
    |||||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1270 AAACACGAGCCAGCTCCAGAAATGCTGCCAAGCTGGAGAGAGTTGAAAGGCACGA 1329
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 71 CTTTCAGCAACGAAACTAAGAGTCAAGGCAATTATACCGAATGCCGACATT 126
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1330 ATTGAATTGTGGGACAGCAACATTCAAAGCATTTATGTGAATGGGCAGAAATT 1385
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

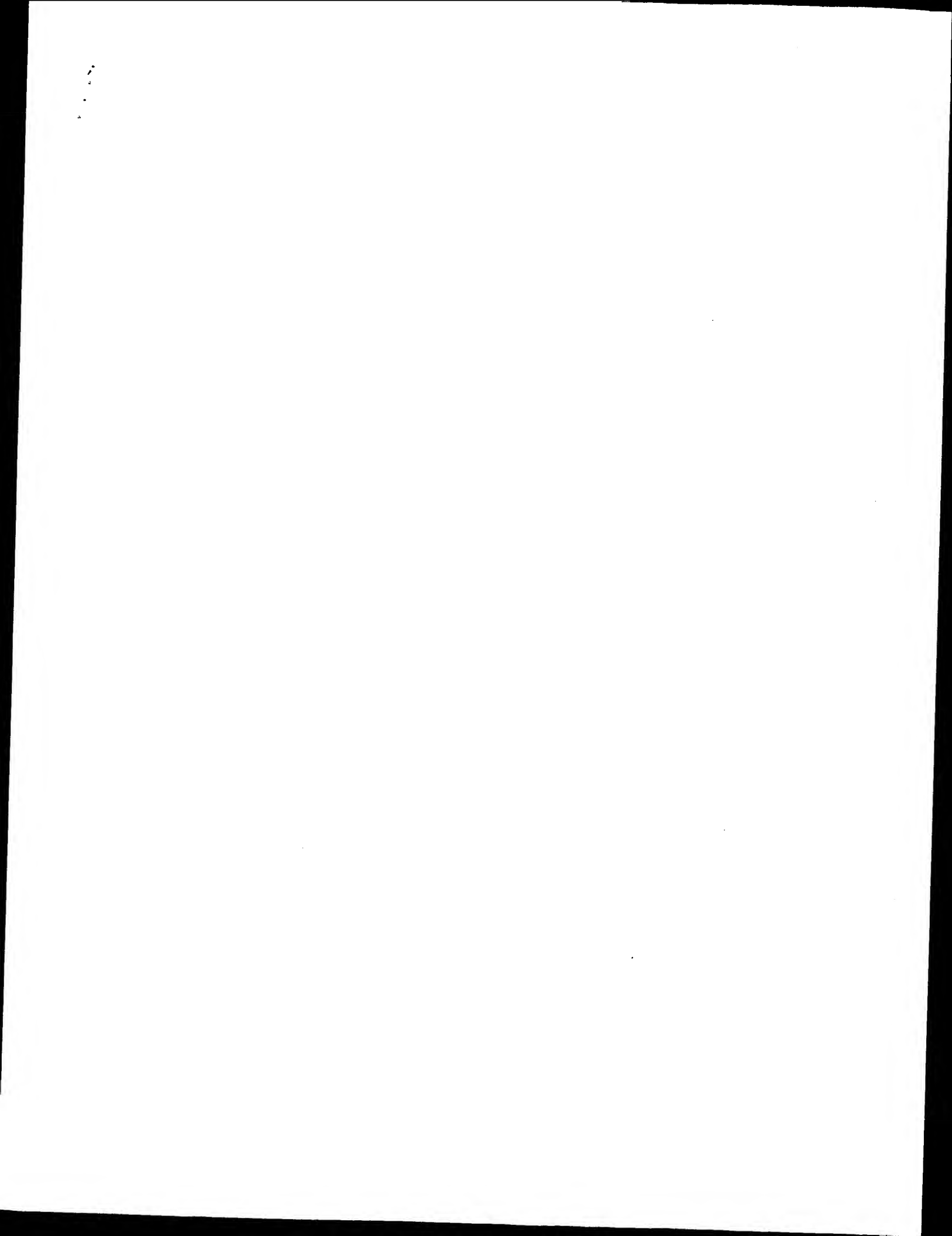
RESULT 15
US-09-920-300A-1690
; Sequence 1690, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1690
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-920-300A-1690

Query Match      15.3%; Score 31.2; DB 10; Length 3073;
Best Local Similarity 54.3%; Pred. No. 0.6; Mismatches 53; Indels 0; Gaps 0;
Matches 63; Conservative 0;

QY 11 ATAAAGGAGCTTTCTTGTGGAACATGACCAAGATTGGGCAACGCTCTCCACATGA 70
    |||||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1270 AAACACGAGCCAGCTCCAGAAATGCTGCCAAGCTGGAGAGAGTTGAAAGGCACGA 1329
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 71 CTTTCAGCAACGAAACTAAGAGTCAAGGCAATTATACCGAATGCCGACATT 126
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1330 ATTGAATTGTGGGACAGCAACATTCAAAGCATTTATGTGAATGGGCAGAAATT 1385
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Search completed: December 8, 2002, 19:38:04
Job time : 18.9188 secs
```



GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:18:27 ; Search time 15.2491 Seconds
(without alignments)
6674.007 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261

Sequence: 1 atggcaatcctgacgctcaag.....gttaattgagaatcattcaac 261

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Published Applications, NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCCT_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	261	100.0	1161	10	US-09-880-457-1
2	251	96.2	1186	10	US-09-880-457-3
3	249.4	95.6	2412	10	US-09-880-457-2
4	121.2	46.4	954	9	US-09-877-650-12
5	121.2	46.4	954	10	US-09-871-856-12
6	118	45.2	1823	9	US-10-017-910-1
7	95.6	36.6	1630	9	US-09-877-650-10
8	95.6	36.6	1630	10	US-09-871-856-10
9	95.6	36.6	2237	9	US-10-017-910-3
10	61	23.4	61	10	US-09-880-457-9
11	33	12.6	454	9	US-09-864-761-14164
12	31.2	12.0	493	9	US-10-040-739-93
13	31.2	12.0	985	10	US-09-920-300A-1691
14	31.2	12.0	985	12	US-10-033-528-1691
15	31.2	12.0	3073	10	US-09-867-701-10910
16	31.2	12.0	3073	10	US-09-920-300A-1690
17	31.2	12.0	3073	12	US-10-033-528-1690
18	30.8	11.8	30310	10	US-09-800-631-96
19	30.4	11.6	53226	10	US-09-818-264-3

C	20	30.2	11.6	2000	10	US-09-887-576-151	Sequence 151, App
C	21	30	11.5	30	10	US-09-880-457-8	Sequence 8, Appl1
C	22	29.6	11.3	2048	10	US-09-764-847-1468	Sequence 1468, App
C	23	29.4	11.3	409	10	US-09-783-590-1953	Sequence 1953, App
C	24	29.4	11.3	2244	10	US-09-764-864-153	Sequence 153, App
C	25	28.8	11.0	257	10	US-09-878-574-7063	Sequence 7063, App
C	26	28.8	11.0	143068	10	US-09-967-768A-316	Sequence 316, App
C	27	28.6	11.0	357	10	US-09-878-574-3028	Sequence 3028, App
C	28	28.6	11.0	407	10	US-09-878-574-3146	Sequence 3146, App
C	29	28.6	11.0	1365	10	US-09-815-242-4243	Sequence 4243, App
C	30	28.6	11.0	1365	10	US-09-815-242-8196	Sequence 8196, App
C	31	28.2	10.8	477	10	US-09-759-143-92	Sequence 92, Appl
C	32	28.2	10.8	477	10	US-09-780-666-92	Sequence 92, Appl
C	33	28.2	10.8	477	10	US-09-030-606-92	Sequence 92, Appl
C	34	28.2	10.8	477	10	US-09-822-827-92	Sequence 92, Appl
C	35	28.2	10.8	477	10	US-09-115-453-92	Sequence 92, Appl
C	36	28.2	10.8	2000	9	US-09-938-842A-4251	Sequence 4251, App
C	37	28	10.7	398	10	US-09-983-965-5848	Sequence 5848, App
C	38	28	10.7	932	10	US-09-925-300-515	Sequence 515, App
C	39	27.8	10.7	666	10	US-09-764-864-590	Sequence 590, App
C	40	27.8	10.7	2147	9	US-09-981-353-104	Sequence 104, App
C	41	27.8	10.7	2222	9	US-09-981-353-76	Sequence 76, Appl
C	42	27.8	10.7	465237	10	US-09-933-267A-1	Sequence 1, Appl
C	43	27.6	10.6	371	10	US-09-834-975-285	Sequence 285, App
C	44	27.6	10.6	486	10	US-09-783-590-10438	Sequence 10438, App
C	45	27.6	10.6	608	10	US-09-759-143-193	Sequence 193, App

ALIGNMENTS

RESULT 1
US-09-880-457-1
Sequence 1, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-1

Query Match 100.0%; Score 261; DB 10; Length 1161;
Best Local Similarity 100.0%; Pred. No. 1.6e-77;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCAATCCTGACGCTGACGCTTCAACATCATCTGTTATTAATACCATCAATATCCCAT	60
DB	486	ATGGCAATCCTGACGCTGACGCTTCAACATCATCTGTTATTAATACCATCAATATCCCAT	545
QY	61	GAGGCTATTAACGATCTCTTCTTGAACATGACCAATGGGCAACGCTCC	120
DB	546	GAGGCTATTAACGATCTCTTCTTGAACATGACCAATGGGCAACGCTCC	605
QY	121	AACATGACTTTCAGACGGAAGAACTAAGATCAAGATTTATTAACCGAATGCCGAC	180
DB	606	AACATGACTTTCAGACGGAAGAACTAAGATCAAGATTTATTAACCGAATGCCGAC	665
QY	181	ATTGCTCTGACATCGCGTACCTGACGAGGCTTAATCTGACGAGCCTTCAGCTATGG	240
DB	666	ATTGCTCTGACATCGCGTACCTGACGAGGCTTAATCTGACGAGCCTTCAGCTATGG	725

QY 241 TGTAAATTTGAGATCATTCAC 261
|||||
Db 726 TGTAAATTTGAGATCATTCAC 746

RESULT 2

US-09-880-457-3
; Sequence 3, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US/09/880,457
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-3

Query Match 96.2%; Score 251; DB 10; Length 1186;
Best Local Similarity 100.0%; Pred. No. 3 6e-74;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAATCCCTGACGCTTCACCTCACTCATCTGTTATTAATACCATCAATATCCCAT 60
|||||
Db 447 ATGGCAATCCCTGACGCTTCACCTCACTCATCTGTTATTAATACCATCAATATCCCAT 506
QY 61 GAGGCTCATATAAAGAGATCTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 120
|||||
Db 507 GAGGCTCATATAAAGAGATCTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 566
QY 121 AACATGACTTTCAGCAACGAGAAACCTAAGATCAAGGCAATTTATTCACGGAATGCCGAC 180
|||||
Db 567 AACATGACTTTCAGCAACGAGAAACCTAAGATCAAGGCAATTTATTCACGGAATGCCGAC 626
QY 181 ATTGCTCTGACATTCGCGTAACCTCGACGAGCCCTAATCTGACGAGACCTTCAGCTATGG 240
|||||
Db 627 ATTGCTCTGACATTCGCGTAACCTCGACGAGCCCTAATCTGACGAGACCTTCAGCTATGG 686
QY 241 TGTAAATTTGAG 251
|||||
Db 687 TGTAAATTTGAG 697

RESULT 3

US-09-880-457-2
; Sequence 2, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US/09/880,457
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-2

Query Match 95.6%; Score 249.4; DB 10; Length 2412;
Best Local Similarity 99.6%; Pred. No. 1.7e-73;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAATCCCTGACGCTTCACCTCACTCATCTGTTATTAATACCATCAATATCCCAT 60
|||||
Db 1784 ATGGCAATCCCTGACGCTTCACCTCACTCATCTGTTATTAATACCATCAATATCCCAT 1843
QY 61 GAGGCTCATATAAAGAGATCTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 120
|||||
Db 1844 GAGGCTCATATAAAGAGATCTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 1903
QY 121 AACATGACTTTCAGCAACGAGAAACCTAAGATCAAGGCAATTTATTCACGGAATGCCGAC 180
|||||
Db 1904 AACATGACTTTCAGCAACGAGAAACCTAAGATCAAGGCAATTTATTCACGGAATGCCGAC 1963
QY 181 ATTGCTCTGACATTCGCGTAACCTCGACGAGCCCTAATCTGACGAGACCTTCAGCTATGG 240
|||||
Db 1964 ATTGCTCTGACATTCGCGTAACCTCGACGAGCCCTAATCTGACGAGACCTTCAGCTATGG 2023
QY 241 TGTAAATTTGAG 251
|||||
Db 2024 TGTAAATTTGAG 2034

RESULT 4

US-09-877-650-12
; Sequence 12, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSER: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

APPLICATION DATA:

APPLICATION NUMBER: US/09/877,650

FILING DATE: 08-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0450

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 954 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-877-650-12

Query Match 46.4%; Score 121.2; DB 9; Length 954;
Best Local Similarity 74.8%; Pred. No. 7.2e-31;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCTGAGCTGACGCTTCACCTTCATCTGTTATTATATACATCAATATCCCATGAG 63
DB 473 GCAGCTTGAGCTGACGCTTCCTTGGCTCATCTATTAATGCCACACATCCCATCTG 532
QY 64 GCT--CATAAACGAGCTCTTCTCTTGTGAACATGACCAAGATTGGGCAACGCTTCCA 121
DB 533 GTTCCCATTAAGTAGCTGCTCTCTTGTGATGATGCGGCTTGGGCAAGATCTCCA 592
QY 122 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 175
QY 176 CCGAGATTGCTCTCGACATGCGGTAACTGACGAGCCCTACTGCGGAGCATCTCAGC 235
DB 653 CCAACATTGCTTTCGACATCATGAACCTTACGAGAGCCTAGCTACAGAGTATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 5
US-09-871-856-12
Sequence 12, Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871.856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-871-856-12

Query Match 46.4%; Score 121.2; DB 10; Length 954;
Best Local Similarity 74.8%; Pred. No. 7.2e-31;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCTGAGCTGACGCTTCACCTTCATCTGTTATTATATACATCAATATCCCATGAG 63
DB 473 GCAGCTTGAGCTGACGCTTCCTTGGCTCATCTATTAATGCCACGACATCCCATCTG 532
QY 64 GCT--CATAAACGAGCTCTTCTCTTGTGAACATGACCAAGATTGGGCAACGCTTCCA 121
DB 533 GTTCCCATTAAGTAGCTGCTCTCTTGTGATGATGCGGCTTGGGCAAGATCTCCA 592
QY 122 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 175
QY 176 CCGAGATTGCTCTCGACATGCGGTAACTGACGAGCCCTACTGCGGAGCATCTCAGC 235
DB 653 CCAACATTGCTTTCGACATCATGAACCTTACGAGAGCCTAGCTACAGAGTATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 6
US-10-017-910-1
Sequence 1, Application US/10017910
Patent No. US2002015970A1
GENERAL INFORMATION:
APPLICANT: Choi, Yongwon
Wong, Brian
Jostien, Ralph
Steinman, Ralph
TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq. David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1823 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-017-910-1

Query Match
Best Local Similarity 45.2%; Score 118; DB 9; Length 1823;
Matches 179; Conservative 0; Mismatches 55; Indels 8; Gaps 2;

QY 4 GCAATTCGAGCTGCTTCAACATCTGTATTATACATCAATATATCCATAG 63
DB 257 GCAAGCTTGAAGCTCTTTTCTGCTCATCTACATTAATGACCGCATCCCATCTG 316
QY 64 GGT--CATTAACGAGCTCTTCTTGTGAAACATGACCAAGATGGGCAACGCTCCA 121
DB 317 GTTCCCATTAAGTGTGCTCTCTGTACCATGATGGGGGTGAGTAACTTCCA 376
QY 122 ACATGACTTTCAGCAACGAAACATAAGATCA-----AAGCATTTATTACCGGAATG 175
DB 377 ACATGACTTTTACGCAATGGAATACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATG 436
QY 176 CCGACATTTGCTTCGACATGCGCTAACCTCAGCAGGCGCTTAAGTCTGAGGAGCCTTACG 235
DB 437 CCAACATTTGCTTTCGACATCATGAACTTCAGAGAGACTTACGAGATATCTTCAAC 496
QY 236 TA 237
DB 497 TA 498

RESULT 7
US-09-877-650-10
Sequence 10, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marasovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <unknown>
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-877-650-10

Query Match
Best Local Similarity 36.6%; Score 95.6; DB 9; Length 1630;
Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps 2;

QY 3 GGCATCTGAGCTCTGACCTTCAACTCATCTTGTATTATTAATACATCAATATCCATGA 62
DB 405 GGCAGCCTGAGGCCGACCATTTGACACCTCACCATCAATGTCGACGATGCCATTCG 464
QY 63 GG--CTCATTAACGAGCTTCTTCTTGAACATGACCAAGATTTGGCAACGCTTCC 120
DB 465 GGTTCCTCATTAAGTCACTCTGCTCTGTACACGATCGAGCTGGGCAAGATCTCT 524
QY 121 AACATGACTTTCAGCAACGAAACATAAGATCA-----AAGCATTTATTACCGGAAT 174
DB 525 AACATGACCTTAAGCAACGAAACTAAGGTTTACCAAGATGGCTTCTATTACCTGTAG 584
QY 175 GCCGACATTTGCTTCGACATGCGCTAACCTCAGCAGGCGCTTAAGTCTGAGGAGCCTTACG 234
DB 585 GCCAACATTTGCTTTCGACATCATTAACATCGGAGAGCTTACGAGACTATCTTCAAG 644
QY 235 CT 236
DB 645 CT 646

RESULT 8
US-09-871-856-10
Sequence 10, Application US/09871856

```

1 Patent No. US20020081720A1
2 GENERAL INFORMATION:
3 APPLICANT: Anderson, Dirk M.
4 Galibert, Laurent
5 Markaskovsky, Eugene
6 TITLE OF INVENTION: Receptor Activator of NF-kappaB
7 NUMBER OF SEQUENCES: 19
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Immunex Corporation, Law Department
10 STREET: 51 University Street
11 CITY: Seattle
12 STATE: WA
13 COUNTRY: USA
14 ZIP: 98101
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: Apple Power Macintosh
19 OPERATING SYSTEM: Apple Operating System 7.5.5
20 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/871,856
23 FILING DATE: 31-May-2001
24 CLASSIFICATION: <unknown>
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/996,139
28 FILING DATE: <unknown>
29 APPLICATION NUMBER: USSN 08/813,509
30 FILING DATE: 07 MARCH 1997
31 APPLICATION NUMBER: USSN 08/772,330
32 FILING DATE: 23 DECEMBER 1996
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Perkins, Patricia Anne
35 REGISTRATION NUMBER: 34,693
36 REFERENCE/DOCKET NUMBER: 2851-A
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (206)587-0430
39 TELEFAX: (206)233-0644
40
41 INFORMATION FOR SEQ ID NO: 10:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 1630 base pairs
44 TYPE: nucleic acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 MOLECULE TYPE: cDNA
48 HYPOTHEICAL: NO
49 ANTI-SENSE: NO
50 ORIGINAL SOURCE:
51 ORGANISM: Mus musculus
52 IMMEDIATE SOURCE:
53 LIBRARY: <Unknown>
54 CLONE: RANKL
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: 3..884
58
59 US-09-871-856-10
60
61 Query Match 36.6%; Score 95.6; DB 10; Length 1630;
62 Best Local Similarity 68.2%; Pred. No.3.2e-22;
63 Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
```

[illegible]

OY	63	GGCTCTAAACAGAGCTTTCTTCTTGGAACATATACCAGAATTGGGCAAGCTCC	120
Dd	670	GGTTCCTTAAGTAGTACTCTCTCTCTTGGTACCATGCATCGAGGCTGGGCCAAGTCTC	729
OY	121	AACATGACTTTCAGCAACGGAAAACTAAGAGTCA-----AAGGCATTATACCGGAAT	174
Dd	730	AACATGAGCTTAAACCAACGGAAAACCTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC	789
OY	175	GCCGACATTTTCTCTCCAGATCGGGTAACTCACACAGGCTTAACCTCTGCAGACCTTCAG	234
Dd	790	GCCACACATTTCTCTTCCGATCATGAAACAATCGGGAAGCGCTACTACAGACTATTCTCAG	849
OY	235	CT 236	
Dd	850	CT 851	

```

RESULT 10 457-9
: US-09-880-457-9
: Sequence 9, Application US/09880457
: Patent No. US20020106728A1
: GENERAL INFORMATION:
: APPLICANT: Pan, James
: APPLICANT: Goddard, Audrey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: NS4 Nucleic Acids and Peptides and Methods of Use
: TITLE OF INVENTION: for the Treatment of Body Weight Disorders
: FILE REFERENCE: P2871R1
: CURRENT APPLICATION NUMBER: US/09/880,457
: CURRENT FILING DATE: 2001-06-12
: PRIOR APPLICATION NUMBER: US 60/212,901
: PRIOR FILING DATE: 2000-06-20
: NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 9
: LENGTH: 61
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Cloning oligonucleotide
: US-09-880-457-9

```

Query Match	23.4%	Score 61	DB 10	Length 61
Best Local Similarity	100.0%	Pred. No. 2.7e-11		
Matches	61	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	132	CAGCAGCGAAATCTAAGCTCAAGCGCTTTATTATTCGCGATCGGACATTTGCTCTCG	191	
Db	1	CAGCAGCGAAATCTAAGCTCAAGCGCTTTATTATTCGCGATCGGACATTTGCTCTCG	60	
QY	192	A	192	
Db	61	A	61	

```

, RESULT 11
, US-09-864-761-14164/C
, Sequence 14164, Application US/09864761
, Patent No. US20020048763A1
, GENERAL INFORMATION:
, APPLICANT: Penn, Sharon G.
, APPLICANT: Rank, David R.
, APPLICANT: Hanzel, David K.
, APPLICANT: Chen, Wensheng
, TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
, TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
, FILE REFERENCE: Aeomica-X-1
, CURRENT APPLICATION NUMBER: US/09/864,761
, CURRENT FILING DATE: 2001-05-23
, PRIOR APPLICATION NUMBER: US 60/180,312
, PRIOR FILING DATE: 2000-02-04
, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 09/632,366

```

```

1  PRIOR FILLING DATE: 2000-08-03
2  PRIOR APPLICATION NUMBER: GB 24263. 6
3  PRIOR FILLING DATE: 2000-10-04
4  PRIOR APPLICATION NUMBER: US 60/236, 359
5  PRIOR FILLING DATE: 2000-09-27
6  PRIOR APPLICATION NUMBER: PCT/US01/00666
7  PRIOR FILLING DATE: 2001-01-30
8  PRIOR APPLICATION NUMBER: PCT/US01/00667
9  PRIOR FILLING DATE: 2001-01-30
10 PRIOR APPLICATION NUMBER: PCT/US01/00664
11 PRIOR FILLING DATE: 2001-01-30
12 PRIOR APPLICATION NUMBER: PCT/US01/00669
13 PRIOR FILLING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: PCT/US01/00665
15 PRIOR FILLING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/00668
17 PRIOR FILLING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/00663
19 PRIOR FILLING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/00662
21 PRIOR FILLING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/00661
23 PRIOR FILLING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00670
25 PRIOR FILLING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: US 60/234, 687
27 PRIOR FILLING DATE: 2000-09-21
28 PRIOR APPLICATION NUMBER: US 09/608, 408
29 PRIOR FILLING DATE: 2000-06-30
30 PRIOR APPLICATION NUMBER: US 09/774, 203
31 PRIOR FILLING DATE: 2001-01-29
32 NUMBER OF SEQ ID NOS: 49117
33 SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
34 SEQ ID NO 14164
35 LENGTH: 454
36 TYPE: DNA
37 ORGANISM: Homo sapiens
38 FEATURE:
39 OTHER INFORMATION: MAP TO AL021307.1
40 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
41 US-09-864-761-14164

```

```

Query Match          12.6%;  Score 33;  DB 10;  Length 454;
Best Local Similarity 50.3%;  Pred. No. 0.15;
Matches      81;  Conservative    0;  Mismatches    80;  Indels    0;  Gaps    0;

QY      41  TAATACCATCAATATATCCATGAGSCTCATATAAAGAGTCTTTCCTTGGAACATGACC 100
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       429  TGAATCTGTTTTTTCACCTATATTAGSCTGACAAATGTTTACTATTTTGTCTACATCATGCGCT 370
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      101  AAGATTGGGCAACGCTCTCCACATGACTTTGAGCAAGCAAGCAACCAAGTCAAGGCA 160
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       369  GAGATTGTGGAGCGCAAAATPACATTTCTCACAACTGCTGTTGGAAACATATATGTAATTT 310
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      161  TTTATTACCGGAATGCGCAGCATTTGCTCTCGACGCGCTA 201
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       309  TCTGTAATTAANAATATACGGCATTTATCTAGCAANAATATAGCTA 269
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-10-040-739-93
; Sequence 93, Application US/10040739
; Patent No. US20020173635A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John
Lavallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
NUMBER OF SEQUENCES: 1519
;
;

```


QY 128 CTTTCAGCAACGAAACTAGAGTCACAAGGCATTATTACCGAATGCCGACATT 183
|||
Db 1330 ATTGAATTGTGGACACGACATTCACAAGGCATTATGCTGATGGCGCAGAAATT 1385

Search completed: December 8, 2002, 19:37:57
Job time : 24.2491 secs

Tue Dec 10 10:51:28 2002

us-09-880-457-1.rnpb

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:18:27 ; Search time 67.8321 Seconds
(without alignments)
6674.007 Million cell updates/sec

Title: US-09-880-457-1
Perfect score: 1161
Sequence: 1 aaagagagataatcaagaa.....taataaagagagaaatgc 1161

Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 19496369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1161	100.0	1161	10	US-09-880-457-1
2	412	35.5	2412	10	US-09-880-457-2
3	268	23.1	1186	9	US-09-880-457-3
4	126	10.9	954	10	US-09-877-650-12
5	122.8	10.6	1823	10	US-09-871-856-12
6	97	8.4	1630	9	US-09-877-650-10
7	97	8.4	1630	9	US-09-871-856-10
8	97	8.4	2237	9	US-10-017-910-3
9	61	5.3	61	10	US-09-880-457-9
10	38	3.3	180216	10	US-09-835-232-6
11	38	3.3	197997	10	US-09-822-246-3
12	35.6	3.1	370	10	US-09-867-701-6187
13	35.6	3.1	495	10	US-09-867-701-10680
14	35.2	3.0	12259	10	US-09-764-869-1690
15	34.2	2.9	606	10	US-09-918-686-9
16	34.2	2.9	51719	10	US-09-918-686-2
17	34.2	2.9	92139	10	US-09-918-686-1
18	33.8	2.9	17761	10	US-09-764-847-1596

20	33.6	2.9	147309	10	US-09-742-312-3	Sequence 3, Appl1
c 21	33.4	2.9	465237	10	US-09-933-267A-1	Sequence 1, Appl1
c 22	33.2	2.9	493	10	US-09-864-761-14364	Sequence 14364, A
c 23	33	2.8	454	10	US-09-864-761-14164	Sequence 14164, A
c 24	33	2.8	4810	10	US-09-764-869-1995	Sequence 1995, Ap
c 25	32.8	2.8	14485	10	US-09-876-216-3	Sequence 1673, Ap
c 26	32.8	2.8	23071	10	US-09-764-864-1673	Sequence 646, App
c 27	32.6	2.8	385	10	US-09-070-927A-646	Sequence 267, App
c 28	32.4	2.8	407	10	US-09-764-869-267	Sequence 4893, Ap
c 29	32.4	2.8	555	10	US-09-783-590-4893	Sequence 15062, A
c 30	32.4	2.8	474	10	US-09-864-761-15062	Sequence 3185, A
c 31	32.4	2.8	529	10	US-09-783-590-3185	Sequence 3727, Ap
c 32	32.2	2.8	22786	10	US-09-864-877-3727	Sequence 3, Appl1
c 33	32.2	2.8	174493	10	US-09-804-471A-3	Sequence 12, Appl1
c 34	31.8	2.7	1371	12	US-10-002-600-12	Sequence 1, Appl1
c 35	31.6	2.7	456	10	US-09-733-523-1	Sequence 245, App
c 36	31.6	2.7	521	9	US-09-924-400-245	Sequence 245, App
c 37	31.6	2.7	521	10	US-09-841-132-595	Sequence 245, App
c 38	31.6	2.7	901	10	US-09-841-132-595	Sequence 595, App
c 39	31.4	2.7	900	10	US-09-841-132-595	Sequence 440, App
c 40	31.4	2.7	2172	10	US-09-822-830A-440	Sequence 469, App
c 41	31.4	2.7	8045	10	US-09-764-887-469	Sequence 292, App
c 42	31.4	2.7	43058	10	US-09-954-456-292	Sequence 3529, App
c 43	31.4	2.7	43058	10	US-09-954-456-292	Sequence 3529, App
c 44	31.4	2.7	43058	10	US-09-880-107-3950	Sequence 3950, App
c 45	31.2	2.7	401	9	US-09-946-807-442	Sequence 442, App

ALIGNMENTS

RESULT 1
US-09-880-457-1
Sequence 1, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-1

Query Match	Score 1161;	DB 10;	Length 1161;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1161;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;
QY 1	AAAAGAGGATATTCAGAGGCGCTTTAAAGGACTATTTCCCAAGATGGAGATGAG 60		
DB 1	AAAAGAGGATATTCAGAGGCGCTTTAAAGGACTATTTCCCAAGATGGAGATGAG 60		
QY 61	GGGAACTGCGAGGCTATGCTTACCTCCAGAGGAGGAGGAGGAGGAGGAGGAT 120		
DB 61	GGGAACTGCGAGGCTATGCTTACCTCCAGAGGAGGAGGAGGAGGAGGAGGAT 120		
QY 121	AAGGACGCGTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 180		
DB 121	AAGGACGCGTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 180		
QY 181	GAGAACCTGCTTGTGAGGCGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAT 240		
DB 181	GAGAACCTGCTTGTGAGGCGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAT 240		

```

QY 241 TTCATCTCTCCCAACCCACAGAGGTTGGTGGGCCCCCAAGGCGAGCTCCGGGGA 300
DB 241 TTCATCTCTCCCAACCCACAGAGGTTGGTGGGCCCCCAAGGCGAGCTCCGGGGA 300
QY 301 GGAAGTGGAGAGAGGAGCTGAGAGGCCAGTGAAGGTATGCACACAGTATCTACAG 360
DB 301 GGAAGTGGAGAGAGGAGCTGAGAGGCCAGTGAAGGTATGCACACAGTATCTACAG 360
QY 361 CACGAGGATTTTGGAGCATTTGGGATTTTGGAGCAACCAAGTGCAGCAAAACCTTG 420
DB 361 CACGAGGATTTTGGAGCATTTGGGATTTTGGAGCAACCAAGTGCAGCAAAACCTTG 420
QY 421 CTCGTGGAGGAGCAATCTTACCAAGGAAGCAATGACACAGAGAGATTTGG 480
DB 421 CTCGTGGAGGAGCAATCTTACCAAGGAAGCAATGACACAGAGAGATTTGG 480
QY 481 TAAGATGGCAATCTGAGCGCTGAGCGCTCAACCTCATCTTGTATTAATCAATAT 540
DB 481 TAAGATGGCAATCTGAGCGCTGAGCGCTCAACCTCATCTTGTATTAATCAATAT 540
QY 541 CCCATGAGGCTCAATTAACAGATCTTCTTCTTGAACATGACCAAGATTGGGCAAG 600
DB 541 CCCATGAGGCTCAATTAACAGATCTTCTTCTTGAACATGACCAAGATTGGGCAAG 600
QY 601 TCTCCAACTGACTTTCAGCAAGGAAACTAGAGTCGAAGGCAATTAATACCGAATG 660
DB 601 TCTCCAACTGACTTTCAGCAAGGAAACTAGAGTCGAAGGCAATTAATACCGAATG 660
QY 661 CCGACATTTGCTCGACATCCGCTTAACCTGAGCGCTTAACCTGAGCGCTTACG 720
DB 661 CCGACATTTGCTCGACATCCGCTTAACCTGAGCGCTTAACCTGAGCGCTTACG 720
QY 721 TATGTGTATTTGAGAATCATCTGAGTCACTGAGTCAATCTATTAACAGCATTTGG 780
DB 721 TATGTGTATTTGAGAATCATCTGAGTCACTGAGTCAATCTATTAACAGCATTTGG 780
QY 781 TCCAGAGATCCAAAGCTTAAGACACCAAAACCTGCTTCCAGGAAACAGAGGGTGA 840
DB 781 TCCAGAGATCCAAAGCTTAAGACACCAAAACCTGCTTCCAGGAAACAGAGGGTGA 840
QY 841 GAGGCCAGCAGAGTGTCTGTCAGTACTTGGAGCGTGAAGAGAGTGGTCTGGGC 900
DB 841 GAGGCCAGCAGAGTGTCTGTCAGTACTTGGAGCGTGAAGAGAGTGGTCTGGGC 900
QY 901 TGAGAGCCAGAGTGTCTGTCAGTACTTGGAGCGTGAAGAGAGTGGTCTGGGC 960
DB 901 TGAGAGCCAGAGTGTCTGTCAGTACTTGGAGCGTGAAGAGAGTGGTCTGGGC 960
QY 961 GGATTTGCATTTTGGATGAATGTGTCTGTCAGTACTTGGAGCGTGAAGAGTGGTCT 1020
DB 961 GGATTTGCATTTTGGATGAATGTGTCTGTCAGTACTTGGAGCGTGAAGAGTGGTCT 1020
QY 1021 CCACAGAGCAAGCATGATGTGATGTCTGTCAGTACTTGGAGCGTGAAGAGTGGTCT 1080
DB 1021 CCACAGAGCAAGCATGATGTGATGTCTGTCAGTACTTGGAGCGTGAAGAGTGGTCT 1080
QY 1081 CCGTGTATTAATCAATCTGTCAGCGCTGGCTATTAATCAATGATGTGTGAAGAGC 1140
DB 1081 CCGTGTATTAATCAATCTGTCAGCGCTGGCTATTAATCAATGATGTGTGAAGAGC 1140
QY 1141 TTAATTAAGGAGGAAATGC 1161
DB 1141 TTAATTAAGGAGGAAATGC 1161

```

```

RESULT 2
US-09-880-457-2
; Sequence 2, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.

```

```

; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-2

```

```

Query Match
Best Local Similarity 35.5%; Score 412; DB 10; Length 2412;
Matches 561; Conservative 0; Mismatches 175; Indels 24; Gaps 2;

```

```

QY 1 AAAGAGATTAATTCAGAGAGGCTTCTTTAAGGACTATTTCCAGAGTGAATGGAG 60
DB 1275 AAAGAGATTAATTCAGAGAGGCTTCTTTAAGGACTATTTCCAGAGTGAATGGAG 1334
QY 61 GGAACCTGCAAGGCTTAATGCTTACCTCCAGCAGGAGGCAATTTCTGAGGGAT 120
DB 1335 GGAACCTGCAAGGCTTAATGCTTACCTCCAGCAGGAGGCAATTTCTGAGGGAT 1394
QY 121 AAGACGTGTGTCAGAGCATGAGAGGAAAGTTCACAGAGAGGACAGTGGGCTTCA 180
DB 1395 AAGACGTGTGTCAGAGCATGAGAGGAAAGTTCACAGAGAGGACAGTGGGCTTCA 1454
QY 181 GGAACCTGCTTGAAGAGGCTTGAAGG--TGGGAAATCAATACCTACCTGCTCT 238
DB 1455 GGAACCTGCTTGAAGAGGCTTGAAGG--TGGGAAATCAATACCTACCTGCTCT 238
QY 239 CTTCCATCTCTCCCAACCCACAGGAGTGTGTGGGCCCAAGGCGAGCTCCGGG 298
DB 1515 AACCTCTTACGCTGTGTGGGAAAGTGTACCCCTGCTCTCCGCTTCTTCTGCACT 1574
QY 299 GAGAGAGTGAAGAGAGGAGCTGAGAGGCCAGTGAAGAGTGAACACAGATATCA 358
DB 1575 CTTGAGCATGTGATGGCTGAGAGGCTGAGAGGCCAGTGAAGAGTGAACACAGAT 1634
QY 359 GGCACAGGCAATTTTGGAGCATTTGGATTTGTACGCAACAGTCAAGCAAAACCT 418
DB 1635 CAGACAGAGCCCTGACATGATGATGCTGGCTGAGAGATCCAGAGAGCCGAGGG 1694
QY 419 TGCTCTGTTGAGGAGCAATTTGTAGCAAAAGGAGCAATATGCAAGC----- 465
DB 1695 GGCACAGGCAATTTGATGCTGGCTGAGCATTTGATGATGATTT 1754
QY 466 -----AGAGAGATTTGCTAAGATGCAATCTGAGCGTCAAGCTTCTGATGATTT 1754
DB 1755 TAATGAGGAGAAAGATATTTGCTTAAGATGCAATCTGATGATGATTT 516
QY 517 TCTGTATTAATTAACATCAATATCCATGAGGCTCAATTAAGAGGCTTCTTCTGGA 576
DB 1815 TCTGTATTAATTAACATCAATATCCATGAGGCTCAATTAAGAGGCTTCTTCTGGA 576
QY 577 AACATGACCAAGATTTGGGCAAGCTTCCAAATGACTTTTCAGCAAGGAAATTAAG 636
DB 1875 AACATGACCAAGATTTGGGCAAGCTTCCAAATGACTTTTCAGCAAGGAAATTAAG 1934
QY 637 TCAAGGCAATTTATTAACGAGATGCGACATTTGCTGAGATGCGGTAACCTGACAG 696
DB 1935 TCAAGGCAATTTATTAACGAGATGCGACATTTGCTGAGATGCGGTAACCTGACAG 1994
QY 697 GCGTAACCTGAGAGGAGCTTACAGTATGCTGATTTTGA 736
DB 1995 GCGTAACCTGAGAGGAGCTTACAGTATGCTGATTTTGA 2034

```

```

RESULT 3
US-09-880-457-3

```

Sequence 3, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO: 3
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-3

Query Match 23.1%; Score 268; DB 10; Length 1186;
Best Local Similarity 100.0%; Pred. No. 3.1e-76;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAAGTATTGCTAAGATGCAATCCGAGCGCTCAGCCTCACTCACTGTTATTAA 528
DB 430 AGAAGTATTGCTAAGATGCAATCCGAGCGCTCAGCCTCACTCACTGTTATTAA 489
QY 529 TACCATCATATCCCATGAGGCTCATAAACGAGCTTTCTTGGAAACATGACCAAG 588
DB 490 TACCATCATATCCCATGAGGCTCATAAACGAGCTTTCTTGGAAACATGACCAAG 549
QY 589 ATTGGCAAGCTCTCCAACTGCTTCCAGCAAGGAAACTAAGAGTCAAGCATTT 648
DB 550 ATTGGCAAGCTCTCCAACTGCTTCCAGCAAGGAAACTAAGAGTCAAGCATTT 609
QY 649 ATTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGAGGCTTAACCTGC 708
DB 610 ATTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGAGGCTTAACCTGC 669
QY 709 AGGACCTCAGTATGTTGTTAATTTGAG 736
DB 670 AGGACCTCAGTATGTTGTTAATTTGAG 697

RESULT 4

US-09-877-650-12

Sequence 12, Application US/09877650
Patent No. US20020169117A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

Application Number: US/09/877,650

Filing Date: 08-Jun-2001

CLASSIFICATION: <Unknown>

Prior Application Data:

Application Number: 08/995,659

FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ANTISENSE: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-877-650-12

Query Match 10.9%; Score 126; DB 9; Length 954;
Best Local Similarity 72.6%; Pred. No. 2.2e-30;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAGTATTGCTAAGATGCAATCTGACGCTCAGCCTTCACTCACTGTTATTAA 524
DB 449 CATGTTAGATCTGGCCCAAGAGAGCAAGCTTGAAGCTCAGCCTTTCATCTCAGTA 508
QY 525 TTAATACCATCAATATCCCATGAGGCT--CATAAACGAGCTTTCTTGGAAACATG 582
DB 509 TTAATGCGACGACATCTGCTGCTCCATTAAGTACGTCTGCTCTTGTACCATG 568
QY 583 ACCAAGATTGGGCAAGCTCTCCAACTGCTTCCAGCAAGGAAACTAAGAGTCA--- 639
DB 569 ATCGGGGTTGGGCCAAGATCTCCAACTGACATTTAGCAATGAAACTAATAGTTATC 628
QY 640 ---AAGCATTTATTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGCAG 696
DB 629 ACGATGCGCTTTATTACCTGTTATGCAACATTTGCTTGGACATCATGAAACTTCAGGAG 688
QY 697 GCCTAAGCTCGAGGACCTTCAGCTA 722
DB 689 ACCTAGCTACAGAGTATCTTCAACTA 714

RESULT 5

US-09-871-856-12

Sequence 12, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

Db 473 ACCTAGCTACAGAGTATCTTCACTA 498

RESULT 7

US-09-877-650-10
Sequence 10, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-877-650-10

Query Match 8.48; Score 97; DB 9; Length 1630;
Best Local Similarity 67.28; Pred. No. 7.3e-21;
Matches 170; Conservative 0; Mismatches 75; Indels 8; Gaps 2;

QY 477 TTGCTAGATGCAATCGACCTGACCTTCACTCATCTTGTATTATATACATCA 536
DB 394 TGGCCACGAGGAGGACCTGAGCCAGCATTTTGCACACCTCATCATCTGTCGA 453
QY 537 ATATCCATGAGG--CTCATTAAGAGGCTTTCTTCTTGAACATGACCAAGATTGG 594

Db 454 GATCCCATCGGGTTCCCATATAAGTCACTGTCTCTTGTACACGATGAGGCTGG 513
QY 595 CAAAGCTCTCCACATGACTTTCAGCAAGGAAACTAAGTGA-----AAGGCA 648
DB 514 CCAAGATCTCTAACAATGACGTTAAGCAAGGAAACTAAGGTTAACCAGATGCTTCT 573
QY 649 ATTACCGGATGCCGACATTTGCTCTGACATCGGCTAACCTCAGAGGCTTAATCTGC 708
DB 574 ATTACCTGACCCCAACTTGTCTTGGCATCATGAAACATCGGGAAGGCTACTACAG 633
QY 709 AGGACCTTCAGCT 721
DB 634 ACTATCTTACGCT 646

RESULT 8

US-09-871-856-10
Sequence 10, Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884

1. STANDARD

61 A 61

[illegible]

RESULT 15
US-09-764-869-1690/c
; Sequence 1690, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ. ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ. ID NO 1690
; LENGTH: 12259
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (398)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-1690

Query Match 3.0%; Score 35.2; DB 10; Length 12259;
Best Local Similarly 51.2%; Pred. No. 2.7;
Matches 82; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 882 CAGGAGTGGGCTGGCTGAGAGACCAAGAGTAATGCGCCCTGGGAGCGCCCGGAGAGA 941
DB 1983 CAGGCTGCAGGTGAGAAAGGCAAGGCTGAGCGCCAGGAGTTGAGAGCCCTAGAGTG 1924
QY 942 GATGAGTTTGTAGGCAAAAGGATTGTCATTTGTGATGAACCTGTGTGTTCACTGAAG 1001
DB 1923 GAACAGCACAGACACTATGCAATTACTCTTAATTATCTTCCGTACAGCTGTGGC 1864
QY 1002 CTGAAGTTGTACTCTGAACCAAGCAAGCAAGCATGATGT 1041
DB 1863 GGTAGCCTGTGCTGTGAGTACAGGTCCAGGTTCCAGCT 1824

Search completed: December 8, 2002, 19:37:48
Job time: 623.832 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 18:34:08 ; Search time 44.7484 Seconds

(without alignments)
313.111 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87

Sequence: 373
1 HEAHTSLSSWKHDQMANV.....TSAGLTLDLQMLNRLRH 68

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mnc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	18.5	214	13	Q9DDZ5
2	69	18.5	1130	15	Q88282
3	68	18.2	187	10	Q9GCA8
4	67	18.0	296	16	Q9X2G7
5	67	18.0	307	10	Q9FT49
6	67	18.0	478	15	Q9T146
7	64.5	17.3	276	16	Q97L30
8	64.5	17.3	1000	4	Q9UB99
9	64.5	17.3	1018	4	Q60350
10	64.5	17.3	1090	4	Q9HC88
11	64.5	17.3	1214	4	Q9Y6M7
12	63.5	17.0	297	5	Q9VCJ9
13	63.5	17.0	813	16	Q913X9
14	63.5	16.9	287	13	Q90WT9
15	62.5	16.8	251	10	Q942B1
16	62	16.6	166	17	Q96ZT5

17	61	16.4	322	5	Q95XD5	Q95XD5 caenorhabdi
18	61	16.4	530	5	Q9YFV1	Q9YFV1 drosophila
19	61	16.4	1101	5	Q45818	Q45818 caenorhabdi
20	61	16.4	1630	16	Q8RH77	Q8RH77 fusobacteri
21	60	16.1	274	16	Q8Y214	Q8Y214 anabena sp
22	60	16.1	354	16	Q8UDK4	Q8UDK4 agrobacteri
23	60	16.1	609	16	Q989R7	Q989R7 rhizobium l
24	60	16.1	2353	16	Q8XTZ4	Q8XTZ4 ralsconia s
25	59.5	16.0	156	17	Q97516	Q97516 salmonella
26	59.5	16.0	216	16	Q8ZK87	Q8ZK87 escherichia
27	59.5	16.0	216	16	Q8XD17	Q8XD17 rhizobium m
28	59.5	16.0	216	16	Q92NK4	Q92NK4 rhizobium m
29	59.5	16.0	427	16	Q9K9G9	Q9K9G9 bacillus ha
30	59	15.8	187	16	Q68768	Q68768 yersinia pe
31	59	15.8	364	16	Q8RF50	Q8RF50 streptomyce
32	58.5	15.7	91	5	Q22506	Q22506 caenorhabdi
33	58.5	15.7	237	2	Q9X6N2	Q9X6N2 streptomyce
34	58.5	15.7	316	4	Q96BW9	Q96BW9 homo sapien
35	58.5	15.7	1171	17	Q97B17	Q97B17 thermoplas
36	58	15.5	308	16	Q8R5V5	Q8R5V5 fusobacteri
37	58	15.5	330	17	Q58765	Q58765 pyrococcus
38	58	15.5	646	10	Q81015	Q81015 arabidopsis
39	57.5	15.4	262	2	Q9FAC1	Q9FAC1 streptomyce
40	57.5	15.4	391	2	Q9UR12	Q9UR12 lactococcus
41	57.5	15.4	425	16	Q9YF22	Q9YF22 streptococ
42	57.5	15.4	729	16	Q921P3	Q921P3 rickettsia
43	57.5	15.4	830	11	Q99LE9	Q99LE9 mus musculi
44	57.5	15.4	1514	5	Q9NBK9	Q9NBK9 drosophila
45	57.5	15.4	1514	5	Q9VUN0	Q9VUN0 drosophila

ALIGNMENTS

RESULT 1

ID	Q9DDZ5	PRELIMINARY;	PRT;	214 AA.
AC	Q9DDZ5;			
DT	01-MAR-2001 (TREMREL. 16, Created)			
DT	01-MAR-2001 (TREMREL. 16, last sequence update)			
DE	01-MAR-2002 (TREMREL. 20, last annotation update)			
GN	TRAIL-like protein.			
OS	Brachydanio rerio (zebrafish) (zebra danio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bohe J., Goetz F.W.;			
RT	"Molecular cloning and expression of a TNF receptor and two TNF			
RT	ligands in the fish ovary."			
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).			
DR	EMBL: AF250041; AAG47640.1; ..			
DR	HSSP: P50591; 1D0G.			
DR	FEIN: ZDB-GENE-010801-1; tnfsf10L.			
DR	InterPro: IPR003636; TNF-abc.			
DR	InterPro: IPR004478; TNF_family.			
DR	Pfam: PF00229; TNF; 1.			
DR	ProDom: PD002012; TNF-abc; 1.			
DR	SMART: SM00207; TNF; 1.			
DR	PROSITE: P550049; TNF-2; 1.			
SQ	SEQUENCE 214 AA; 24093 MW; 98C00247AFF691AA CRC64;			

Query Match Best Local Similarity 31.2%, Score 69; DB 13; Length 214; Matches 15; Conservative 13; Mismatches 18; Indels 2; Gaps 1;

QY 1 HEAHTSLSSWKHDQMANVSNFSGNCKLRV--KGIYRNADICSRH 46
DB 76 HOSCHRPVHTWANKSFGAHLNMTLTNRLRVPDGRITLYISQYFERY 123

[illegible]

```

OY 1 HEAKTSLSSMKHODM-----ANVSNMFTSNGKLRVKGIIYRN 39
DB 149 HDEKYLSTFWIRNKKVRSHEHVLVIGARTSMKKTCCHIHLPYSOG-ITINGVLTYG 207
OY 40 ADICSRHRTVSAGLTLODLQW 61
DB 208 AWDDKCVLMSFDLTSDEYGVW 229

RESULT 6
OY 071146 PRELIMINARY: PRT: 478 AA.
ID 071146:
AC 071146:
DB 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENVELOPE glycoprotein gp120 (Fragment).
ENV.
GN Human immunodeficiency virus type 1.
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=V22
RC MEDLINE=96039896; PubMed=7576917;
RA Quinones-Mateu M.E., Esté J.A., Rota T.R., Domingo E.;
RT "Molecular characterization of human immunodeficiency virus type 1
RT isolates from Venezuela."
RL AIDS Res. Hum. Retroviruses 11:605-616(1995).
RU AIDS Res. Hum. Retroviruses 11:605-616(1995).
RV [2]
RW SEQUENCE FROM N.A.
RX STRAIN=VE2;
RC MEDLINE=97000986; PubMed=8844016;
RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
RT "Point mutant frequencies in the pol gene of human immunodeficiency
RT virus type 1 are two- to threefold lower than those of env."
RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
RU EMBL: 016766; AAC55683.1;
DR Interpro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; glycoprotein.
FT NON_TER 1 478
FT SEQUENCE 478 AA; 53554 MW; 103F636765B51D92 CRC64;
SQ
Query Match 18.0%; Score 67; DB 15; Length 478;
Best Local Similarity 25.0%; Pred. No. 5.5; 27; Indels 24; Gaps 3;
Matches 21; Conservative 12; Mismatches 127

OY 2 EAHKTSLSMKHODM-----DMANVSNMFTSNGKLRVKGIIYRNADIC 43
DB 74 QMHEITISLW--DOSIKRCVKLPLCYLCTDCTDMGNATNTNISGGAMERG----EIKNC 127
OY 44 SRHRTVSAGLTLODLQW 61
DB 128 SFNITTSSEKMKREALTYNDV 151

RESULT 7
OY 097130 PRELIMINARY: PRT: 276 AA.
ID 097130:
AC 097130:
DB 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Possible glucanotransferase (putative endo alpha-1,4
DE polygalactosaminidase related protein).
GN CA00736.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_Taxid=1488;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=1146286;
RA Noselling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Hiti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RA bacterium Clostridium acetobutylicum."
RT J. Bacteriol. 183:4823-4838(2001).
RL EMBL: AE007588; AAK78712.1;
DR Transferrase; Complete proteome.
KW SEQUENCE 276 AA; 32104 MW; 2EFC06A7E4791B CRC64;
SQ
Query Match 17.3%; Score 64.5; DB 16; Length 276;
Best Local Similarity 30.5%; Pred. No. 5.9; 15; Indels 11; Gaps 4;
Matches 18; Conservative 15; Mismatches 15;

OY 10 SMKRDQMANVSNMFTSN-----GK-LRVKGI---YRNADICSRHRTVSAGLTLODL 58
DB 105 NWK-DESMIDVSNLKMNYVNTLGRNKKGVDFDNDVYSKYKKDSMFIGLINI 162

RESULT 8
OY 0901B9 PRELIMINARY: PRT: 1000 AA.
ID 0901B9:
AC 0901B9:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
ENVELOPE glycoprotein gp120 (Fragment).
ENV.
GN Human immunodeficiency virus type 1.
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=V22
RC MEDLINE=96039896; PubMed=7576917;
RA Quinones-Mateu M.E., Esté J.A., Rota T.R., Domingo E.;
RT "Molecular characterization of human immunodeficiency virus type 1
RT isolates from Venezuela."
RL AIDS Res. Hum. Retroviruses 11:605-616(1995).
RU AIDS Res. Hum. Retroviruses 11:605-616(1995).
RV [2]
RW SEQUENCE FROM N.A.
RX STRAIN=VE2;
RC MEDLINE=97000986; PubMed=8844016;
RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
RT "Point mutant frequencies in the pol gene of human immunodeficiency
RT virus type 1 are two- to threefold lower than those of env."
RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
RU EMBL: 016766; AAC55683.1;
DR Interpro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; glycoprotein.
FT NON_TER 1 478
FT SEQUENCE 478 AA; 53554 MW; 103F636765B51D92 CRC64;
SQ
Query Match 17.3%; Score 64.5; DB 4; Length 1000;
Best Local Similarity 32.2%; Pred. No. 28; 17; Indels 11; Gaps 5;
Matches 19; Conservative 12; Mismatches 17;

OY 7 SLSMKHODQMA-NVS--NMFTSNGKLRVKGIIYRNADICSRHRTVSAGLTLODLQW 62
DB 564 TLAQMKNDITANISRNLTVESEK-KLRGVFLSA--CGHH-----GPIYPOVLEWMC 614

RESULT 9
OY 060350 PRELIMINARY: PRT: 1018 AA.
ID 060350:
AC 060350:
DB 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sodium bicarbonate cotransporter2.
GN SBC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 17:28:38; Search time 12.7226 Seconds

(without alignments)
221.684 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAHKTSLSMKHDDMANV.....TSAGLTLDLQMLNRIH 68

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	47.7	317	1	TN11_HUMAN
2	175	46.9	318	1	TN11_RAT
3	172	46.1	316	1	TN11_MOUSE
4	63.5	17.0	263	1	PYRF_PICAN
5	61.5	16.5	501	1	CSD2_DROME
6	59.5	16.0	216	1	SGAH_ECOLI
7	59.5	16.0	329	1	IPNS_MOUSE
8	58.5	15.7	251	1	Y108_CHLTR
9	58.5	15.7	269	1	IL1B_TRIUV
10	58.5	15.5	119	1	YRAN_HAELN
11	57.5	15.4	478	1	DISR_AGRH
12	57.5	15.4	677	1	RNI4_YEAST
13	57.5	15.4	2156	1	RPI_HUMAN
14	56.5	15.1	404	1	FCG1_MOUSE
15	56.5	15.0	196	1	TRAP_ECOLI
16	56.5	15.0	484	1	SLT2_YEAST
17	56.5	15.0	785	1	APR2_YEAST
18	55.5	14.9	144	1	IAAE_HORVU
19	55.5	14.9	680	1	KALM_HUMAN
20	55.5	14.9	837	1	TP11_HUMAN
21	55.5	14.7	500	1	CP11_RABIT
22	54.5	14.6	310	1	SC65_YARLI
23	54.5	14.6	333	1	IPNS_STRLP
24	54.5	14.6	855	1	ENV_HV1A2
25	54.5	14.6	1451	1	SPT6_YEAST
26	54.5	14.5	261	1	TNPF_AOTTR
27	54.5	14.5	261	1	TNPF5_CALCIA
28	54.5	14.5	261	1	TNPF5_HUMAN
29	54.5	14.5	261	1	TNPF5_MACMU
30	54.5	14.5	318	1	ATPS_YEAST
31	54.5	14.5	851	1	NDU1_YEAST
32	54.5	14.5	886	1	ORC1_KLUDA
33	53.5	14.3	329	1	IPNS_STRUP

34	53.5	14.3	2255	1	RRPL_SVS	Q08434 simlan viru
35	53	14.2	220	1	PIS_YEAST	P06197 saccharomyc
36	53	14.2	334	1	GUB_CLOTM	P29716 clostridium
37	53	14.2	377	1	PROB_MEIRU	O92598 meliothermus
38	53	14.2	453	1	PPAL_SCHPO	P08091 schizosacch
39	53	14.2	475	1	PRTG_ERWCH	O07162 erwinda chr
40	53	14.2	636	1	SGA7_HUMAN	O99884 homo sapien
41	53	14.2	764	1	PAG_BACAN	P13423 bacillus an
42	53	14.2	869	1	POZ1_SCICO	P20043 lactobacill
43	53	14.2	1006	1	BCAL_IACDE	O13683 schizosacch
44	53	14.2	1237	1	VDY2_SCHPO	Q03834 saccharomyc
45	53	14.2	1242	1	MSH6_YEAST	

ALIGNMENTS

RESULT 1
ID TN11_HUMAN STANDARD: PRT: 317 AA.
AC 014788: 014723; Q9P203; Q96Q17;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast
DE differentiation factor) (ODF).
CN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=bone marrow, and peripheral blood;
RC MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP TISSUE=Lymph node;
RC MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RP TISSUE=Thymocytes;
RC MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Aron J., Robinson E., Orlicki J., Chao M.,
RA Kalachikov S., Cayan E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [5]
RP TISSUE=Tongue;
RC SEQUENCE FROM N.A. (ISOFORM 2).
RN [5]
RP TISSUE=Tongue;

CC TRABECULAR BONE AND LUNG.
 CC -1- PTH: N-glycosylated
 CC -1- PTH: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -1- DISEASE: DEFICIENCY IN TNFSF1 RESULTS IN FAILURE TO FORM LOBULO-
 CC OF MEMBRANES. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS WITH
 CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
 CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
 CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
 CC HYPERTROPHIC CHONDROCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL, AF013170; AAC71061.1;
 CC EMBL, AF019048; AAB66812.1;
 CC EMBL, AF053713; AAC40113.1;
 CC EMBL, AB008426; BAA35425.1;
 CC EMBL, AB022039; BAA36970.1;
 CC EMBL, AB022036; BAA36970.1;
 CC EMBL, AB022037; BAA36970.1;
 CC EMBL, AB022038; BAA36970.1;
 CC EMBL, AB032771; BAA97257.1;
 CC EMBL, AB032772; BAA97257.1;
 CC EMBL, AB036798; BAA97259.1;
 CC PDB: 1J7E; 13-SEP-01.
 CC PDB: 1J7E; 13-MAR-02.
 CC MGI: 1100089; Tnfrsf11.
 CC InterPro: IPR003636; TNF_family.
 CC Pfam: PF00229; TNF; 1.
 CC SMART: SMO0207; TNF; 1.
 CC PROSITE: PS00251; TNF_1; FALSE_NEG.
 CC PROSITE: PS50049; TNF_2; 1.
 CC Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 CC Signal-anchor; 3D-structure; 316
 CC CHAIN 1 316
 CC FT CHAIN 139 316
 CC FT DOMAIN 1 48
 CC FT TRANSMEM 49 69
 CC FT
 CC FT DOMAIN 70 316
 CC FT SITE 138 139
 CC FT CARBOHYD 197 197
 CC FT CARBOHYD 262 262
 CC FT VARSPLIC 1 117
 CC FT VARSPLIC 14 44
 CC FT
 CC FT CONFLICT 99 99
 CC FT CONFLICT 141 143
 CC FT SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;
 CC
 CC Query Match 46.18; Score 172; DB 1; Length 316;
 CC Best Local Similarity 56.7%; Pred. No. 4.4e-14;
 CC Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;
 CC
 CC 3 AHTYSSWKKHODMANVSMFNSGKLYRK--GIYRNADICSHRYTSAGLTLQDL 60
 CC Db 178 SHKVTLSWYHDGMAKISNMLTSGKLVKLVNODGFYUAVANICFHHFTSSGVPPIYQL 237
 CC RESULT 4

PYRE_PICAN
 ID PYRE_PICAN STANDARD; PRT; 263 AA.
 AC Q06375;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
 DE (OMPDecase) (OMPDecase) (Uridine 5'-monophosphate synthase) (UMP
 DE synthase).
 GN URA3.
 OS Pichia angusta (Yeast) (Hansenula polymorpha).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94128354; PubMed-7764392;
 RA Merckelbach A., Goedecke S., Janowicz Z.A., Hollenberg C.P.,
 RA "Cloning and sequencing of the ura3 locus of the methylothrophic yeast
 RA Hansenula polymorpha and its use for the generation of a deletion by
 RA gene replacement".
 RL Appl. Microbiol. Biotechnol. 40:361-364(1993).
 CC -1- CATALYTIC ACTIVITY: Orotidine 5'-phosphate -> UMP + CO(2).
 CC -1- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
 CC -1- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL, X69461; CAA49221.1;
 CC PIR: S31323; S31323.
 CC DR HSP: P03962; IDGW.
 CC DR InterPro: IPR001754; OMPDecase.
 CC DR Pfam: PF00215; OMPDecase; 1.
 CC DR PROSITE: PS00156; OMPDecase; 1.
 CC KM Pyrimidine biosynthesis; Lyase; Decarboxylase.
 CC FT ACT_SITE 92
 CC FT SEQUENCE 263 AA; 29275 MW; 0934EF673B03A820 CRC64;
 CC
 CC Query Match 17.0%; Score 63.5; DB 1; Length 263;
 CC Best Local Similarity 39.5%; Pred. No. 1.2;
 CC Matches 17; Conservative 7; Mismatches 12; Indels 7; Gaps 2;
 CC
 CC 14 DQDMANVSMFTSNGKLYRKGIYRN--ADICSHRYTSAGL 53
 CC Db 90 DRKFADIGNTV---KLYKGGIYRTSKWADITNAHGYTAGI 128
 CC RESULT 5
 CC CSQ2_DROME
 CC ID CSQ2_DROME STANDARD; PRT; 501 AA.
 CC AC Q9YWT6;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DE 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DE Probable cytochrome P450 2B42 (EC 1.14.14.1) (CYP2B42).
 CC GN CYP2B42 OR CG6081.
 CC OS Drosophila melanogaster (Fruit fly).
 CC OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC STRAIN=Berkley;
 CC MEDLINE-20196006; PubMed-10731132;
 CC RA Adams M.D., Celinkner S.E., Holt R.A., Evans C.A., O'Carroll J.D.,
 CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Tandell M.D., Zhang Q., Chen L.X.,
 Brannon G.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,
 Jallat M., Kalish C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos A.C., Stapleton M., Strong R., Smith T.,
 Spier E., Spreading A.C., Turner R., Venter E., Wang A.H., Wang X.,
 Svirskas R., Tector C., Turner R., Venter E., Weissbach J.,
 Wang Z.-Y., Wasserman D.A., Weinstock K.C., Wu D., Yang S., Yao Q.A.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu S., Zhu X., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).

CONCEPTUAL TRANSLATION.

Unpublished observations (SEP-2000).
 IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 oxidized flavoprotein + H(2)O.
 -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
 (potential).
 -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
 gene model prediction.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

CC EMBL: AEO03609; AAF52225.1; ALT-SPQ.
 CC DR FLYBASE: FBgn0031688; CYP28A2.
 CC DR InterPro: IPR001128; Cytochrome_P450.
 CC DR Pfam: PF00067; P450; 1.
 CC DR PRINTS: PR00385; P450.
 CC DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 CC DR Oxidoreductase: Monooxygenase; Membrane; Heme; Microsome;
 KW Endoplasmic reticulum; Hypothetical protein.
 KW BINDING 446 446 HEME (BY SIMILARITY).
 FT SEQUENCE 501 AA; 36222 MW; 9AD85F249390A655 CRC64;

Query Match 16.5%; Score 61.5; DB 1; Length 501;
 Best Local Similarity 20.8%; Pred. No. 4.6;
 Matches 21; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

OY 1 HEAHTISLSSKKHODMANVSN---MTFSNGKL-----RVKCI 35
 DB 93 HRYATDPRSP-HNNEMRNFKKTDMLGNNPVLGDGDKERRSRIMPALSPNRYKAV 151
 OY 36 YYRNADICSR-----HRYTSAGLTLDOLQMCNIRII 67
 DB 152 YEVSOVCCKFEFYIRPOQOMATSEGLDAMDLSICYTEEV 192

RESULT 6

SCAH_ECOLI STANDARD; PRT; 216 AA.
 AC P39304;
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Probable hexulose 6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino
 DE 3-hexulose 6-phosphate formaldehyde lyase).
 OS SCAH OR B4196.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP SFRAIN-K12 / MG1655;
 RC MEDLINE=9534362; PubMed=7610040;
 RX Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 Blattner F.R.;
 RA "Analysis of the *Escherichia coli* genome VI: DNA sequence of the
 RA region from 92.8 through 100 minutes.";
 RT Nucleic Acids Res. 23:2105-2119(1995).

[2]
 DISCUSSION OF SEQUENCE.
 RA Reizer J., Charbit A., Reizer A., Sailer M.H. Jr.;
 RT "Novel phosphotransferases system genes revealed by bacterial genome
 RT analysis: operons encoding homologues of sugar-specific permease
 RT domains of the phosphotransferase system and pentose catabolic
 RT enzymes.";
 RT Genome Sci. Technol. 1:53-75(1996).

[3]
 DISCUSSION OF SEQUENCE.
 RP MEDLINE=97419490; PubMed=9274005;
 RX Reizer J., Reizer A., Sailer M.H. Jr.;
 RA "Is the ribulose monophosphate pathway widely distributed in
 RT bacteria?"
 RT Microbiology 143:2519-2520(1997).
 RL Microbiology 143:2519-2520(1997).
 CC -1- FUNCTION: CONDENSATION OF D-RIBULOSE 5-PHOSPHATE WITH FORMALDEHYDE
 CC TO FORM D-ARABINO-6-HEXULOSE 3-PHOSPHATE.
 CC -1- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
 CC SGAH AND SGAE.

CC -1- SIMILARITY: BELONGS TO THE HUMPS FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

CC EMBL: U14003; AAA97092.1;
 CC DR EMBL: AEO00491; AAC77153.1;
 CC DR SWISS-2DPAGE: P39304; COLI.
 CC DR Ecocyc: EGI2496; sgaH.
 CC DR InterPro: IPR001754; OmpDecase.
 CC DR Pfam: PF00215; OmpDecase; 1.
 KW Lyase; Complete proteome.
 KW SEQUENCE 216 AA; 23578 MW; EC8490DA1D020824 CRC64;

Query Match 16.0%; Score 59.5; DB 1; Length 216;
 Best Local Similarity 23.6%; Pred. No. 3.1;
 Matches 17; Conservative 16; Mismatches 28; Indels 11; Gaps 3;

```

      1 HEARTSSWMD-----ODMANSNTFS-NKLEFKCIYYRNDICSRHRTSA 51
      : | | | | | : | : | | | | : | : |
      : | | | | | : | : | | | | : | : |

```

	RESULT 9	
IL1B_TRIVU		
D IL1B_TRIVU	STANDARD;	PRT; 269 AA.
C Q9X577;		
T 15-JUN-2002 (Rel. 41, Created)		
T 15-JUN-2002 (Rel. 41, Last sequence update)		
T 15-JUN-2002 (Rel. 41, Last annotation update)		
E Interleukin-1 beta precursor (IL-1 beta).		
N IL1B.		
S Trichosurus vulpecula (Brush-tailed possum).		
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
C Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.		
C NCBI_TaxID=9337;		

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M73461; AAA21300.1; -;
 DR EMBL: Z48703; CA889771.1; -;
 DR PIR: A40257; A40257.
 DR SGD: S0004665; RNA14.
 DR InterPro: IPR003107; HAT.
 DR SMART: SM00386; HAT; 3.
 KW mRNA processing; Nuclear protein; Repeat.
 FT REPEAT 56 88 HAT 1.
 FT REPEAT 90 124 HAT 2.
 FT REPEAT 138 170 HAT 3.
 FT REPEAT 181 214 HAT 4.
 FT REPEAT 257 289 HAT 5.
 FT REPEAT 298 330 HAT 6.
 SQ SEQUENCE 677 AA; 79960 MW; 102433295FE7CD63 CRC64;

Query Match 15.4%; Score 57.5; DB 1; Length 677;
 Best Local Similarity 30.6%; Pred. No. 21;
 Matches 15; Conservative 9; Mismatches 20; Indels 5; Gaps 1;

OY 15 ODMANVSMFTSNCKLRKYGITYRNADICSRHRTVSAGLTLDIOLMCN 63
 DB 239 QEWLNV-----TNGIKRASPINLTANKKNIPQPTSDSNIOQLIWLN 282

RESULT 13
 ID RPL_HUMAN STANDARD; PRT; 2156 AA.
 AC P56715;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Oxygen-regulated protein 1 (retinitis pigmentosa Rpl protein)
 DE (Retinitis pigmentosa 1 protein).
 GN RPL OR ORPL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS HIS-872; TYR-985; THR-1670; PRO-1691
 RP AND TYR-2033.
 RC TISSUE=Retina;
 RX MEDLINE=99318096; PubMed=10391212;
 RA Sullivan L.S., Heckenlively J.R., Bowne S.J., Zuo J., Hide W.A.,
 RA Gal A., Denton M., Inglehearn C.F., Blanton S.H., Dalgner S.P.;
 RT "Mutations in a novel retina-specific gene cause autosomal dominant
 RT retinitis pigmentosa.";
 RL Nat. Genet. 22:255-259(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=99318095; PubMed=10391211;
 RA Pierce E.A., Quinn T., Meenan T., McGee T.L., Berson E.L., Dryja T.P.;
 RT "Mutations in a gene encoding a new oxygen-regulated photoreceptor
 RT protein cause dominant retinitis pigmentosa.";
 RL Nat. Genet. 22:248-254(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99310563; PubMed=10401003;
 RA Guillonneau X., Pflieger N.I., Danciger M., Kozak C.A., Cideciyan A.V.,
 RA Jacobson S.G., Farber D.B.;
 RT "A nonsense mutation in a novel gene is associated with retinitis
 RT pigmentosa in a family linked to the RPL locus.";
 RL Hum. Mol. Genet. 8:1541-1546(1999).
 CC -1- FUNCTION: COULD HAVE A ROLE IN THE DIFFERENTIATION OF
 CC PHOTORECEPTOR CELLS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN RETINA. NOT EXPRESSED IN HEART,
 CC BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, SPLEEN AND

CC PANCREAS.
 CC -1- DISEASE: DEFECTS IN RPL CAUSE RETINITIS PIGMENTOSA FORM 1 (RPL); A
 CC DISEASE CHARACTERIZED BY CONSTRUCTION OF THE VISUAL FIELDS, NIGHT
 CC BLINDNESS, AND FUNDS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED
 CC WITH TRUNCATED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
 CC PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS.
 CC -1- DATABASE: NAME=Retnet;
 CC NOTE=Retinal information network;
 CC WWW="http://www.sph.utmc.edu/retnet/";
 CC DATABASE: NAME=Mutations of the RPL gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/rplmut.htm".

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: AF143226; AAD44197.1; -;
 DR EMBL: AF143224; AAD44197.1; JOINED.
 DR EMBL: AF143225; AAD44197.1; JOINED.
 DR EMBL: AF143222; AAD44198.1; -;
 DR EMBL: AF141021; AAD42072.1; -;
 DR EMBL: AF152242; AAD46774.1; -;
 DR EMBL: AF152240; AAD46774.1; JOINED.
 DR EMBL: AF152241; AAD46774.1; JOINED.
 DR EMBL: AF146592; AAD46769.1; -;
 DR GeneW: HGNC:10263; RPL.
 DR MIM: 603937; -;
 DR MIM: 180100; -;
 DR InterPro: IPR003533; DCX.
 DR Pfam: PF03607; DCX; 2.
 DR SMART: SM00537; DCX; 2.
 KW PROSITE: PS50309; DC; 2.
 KW Vision: Retinitis pigmentosa; Polymorphism; Repeat.
 FT DOMAIN 36 118 DOUBLECORTIN 1.
 FT DOMAIN 154 233 DOUBLECORTIN 2.
 FT DOMAIN 268 273 POLY-SER.
 FT DOMAIN 671 675 POLY-LYS.
 FT DOMAIN 1687 1691 POLY-SER.
 FT VARIANT 872 872 R->H.
 FT VARIANT 985 985 /FTId=VAR_007810.
 FT VARIANT 1670 1670 N->Y.
 FT VARIANT 1670 1670 /FTId=VAR_007811.
 FT VARIANT 1691 1691 A->T.
 FT VARIANT 1691 1691 /FTId=VAR_007812.
 FT VARIANT 2033 2033 S->P.
 FT VARIANT 2033 2033 /FTId=VAR_007813.
 FT VARIANT 2033 2033 C->Y.
 SQ SEQUENCE 2156 AA; 240659 MW; 55AEDECA3DA507 CRC64;

Query Match 15.4%; Score 57.5; DB 1; Length 2156;
 Best Local Similarity 28.8%; Pred. No. 81;
 Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

OY 6 TSLSMKHHDDPMANVSMFTSNCKLRKYGITYRNADICSRHRTVSAGLTLD 57
 DB 666 SSVASKKKKKRSQAINSRYDGLAIKGIINKNERINTKRTKE-MIVYD 716

RESULT 14
 ID FCGL_MOUSE STANDARD; PRT; 404 AA.
 AC P26151;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE High affinity immunoglobulin gamma FC receptor 1 precursor (FC-gamma

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 19:27:28 ; Search time 22.8129 Seconds
(without alignments)
286.555 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEHKTSLSSWKHDQDMANV.....TSAGLTLDLQMLCNRRIH 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	18.0	296	2 E72203	conserved hypothet
2	67	18.0	307	2 T46103	hypothetical prote
3	64.5	17.3	276	2 E96990	probable glucanotr
4	63.5	17.0	263	1 S31323	orotidine-5'-phosp
5	63.5	17.0	813	2 F83476	probable sideropho
6	61	16.4	1101	2 T20881	hypothetical prote
7	60	16.1	274	2 AC1866	glycosyl hydrolase
8	60	16.1	283	2 AT2835	hypothetical 32.0K
9	60	16.1	354	2 C97614	probable hexulose-
10	59.5	16.0	216	2 S56421	probable hexulose-
11	59.5	16.0	216	2 D91275	probable hexulose-
12	59.5	16.0	216	2 DB6116	isopenicillin N sy
13	59.5	16.0	329	2 A29894	acetylornithine de
14	59.5	16.0	427	2 F83984	hypothetical prote
15	59	15.8	187	2 T15023	hypothetical prote
16	58.5	15.7	91	2 T29796	hypothetical prote
17	58.5	15.7	251	2 C71557	probable ACR - Chl
18	58	15.5	119	2 C64174	hypothetical prote
19	58	15.5	330	2 C71096	probable modifcat
20	58	15.5	466	2 T02643	hypothetical prote
21	57.5	15.4	478	2 T01301	hemorrhagic protei
22	57.5	15.4	677	2 S54561	RNA14 protein - ye
23	57.5	15.4	729	2 A97747	oligopeptidase B (
24	57.5	15.4	1063	2 S18211	hypothetical prote
25	57	15.3	345	2 D97407	hypothetical prote
26	57	15.3	345	2 AE2625	conserved hypothet
27	57	15.3	398	2 AC1998	hypothetical prote
28	56.5	15.1	216	2 AB1052	probable hexulose-
29	56.5	15.1	280	2 I55577	Fc gamma (19c) rec

30	56.5	15.1	404	2 A46480	Fc gamma (19c) rec
31	56.5	15.1	920	2 C96831	hypothetical prote
32	56.5	15.1	2167	2 T34395	hypothetical prote
33	56	15.0	350	2 S70135	hypothetical prote
34	56	15.0	484	2 S43737	protein kinase SLT
35	56	15.0	785	2 S73098	aminopeptidase (EC
36	56	15.0	788	2 AF0122	probable membrane
37	56	15.0	1327	2 B90674	AldA-I adhesin-lik
38	56	15.0	1349	2 E85524	probable beta-bar
39	55.5	14.9	148	1 T1BH	trypsin inhibitor
40	55.5	14.9	336	2 T48471	Fc gamma (19c) rec
41	55.5	14.9	469	2 T09366	cytochrome P450 ho
42	55.5	14.9	679	2 A40351	adhesion-type prot
43	55.5	14.9	680	2 S17982	Kallmann syndrome
44	55.5	14.9	760	2 T06291	extensin homologue
45	55.5	14.9	837	2 T12531	hypothetical prote

ALIGNMENTS

RESULT 1

E72203 conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: E72203

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: E72203

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-296 <ARN>

A:Cross-references: GB:AE001822; GB:AE000512; NID:94982429; PIDN:AAD36914.1; PID:9498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1852

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1107

Query Match

Best Local Similarity 27.3%; Pred. No. 2.2;

Matches 15; Conservative 11; Mismatches 19; Indels 10; Gaps 3;

QY 14 DDDM---ANVSNMTFSGKLRVKG---IYRNADICSRHRTSAGLTLDLQMC 62

DB 244 EDMEKFGGVNVVPSDAMIEYGYVYGGADNC-----IALATIPVEKVMKC 294

RESULT 2

T46103 hypothetical protein T25B15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46103

R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Maché, R.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, January 2000

A:Reference number: 223021

A:Accession: T46103

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-307 <ALC>

A:Cross-references: EMBL:AL132972
A:Experimental source: cultivar Columbia; BAC clone T25B15
C:Genetics:
A:Map position: 3
A:Introns: 63/3; 225/2; 267/3
A:Note: T25B15.100

Query Match 18.0%; Score 67; DB 2; Length 307;

Best Local Similarity 18.3%; Pred. No. 2.3;
Matches 15; Conservative 19; Mismatches 26; Indels 22; Gaps 2;

OY 1 HEHKTSLSSMKHDDOM-----ANVSMTFSNGKLRVKGIYRN 39
DB 149 HDYKYLSTFWIRNKMKRSEHHVVLVGARTSMKTKOCHIHLPYSG-ITINGVLYYG 207

OY 40 ADICSRHRYTSAGLTQDLOLW 61
DB 208 AWTDDKCVLMSFDTSEDEYGVW 229

RESULT 3

E96990

Probable glucanotransferase (endo alpha-1,4 polygalactosaminidase related protein) [imp]

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: E96990

R:Noilling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: E96990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-276 <KOR>

A:Cross-references: GB:AE001437; PIDN:AAK78712.1; PID:915023617; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0736

Query Match

Best Local Similarity 17.3%; Score 64.5; DB 2; Length 276;
Matches 18; Conservative 15; Mismatches 15; Indels 11; Gaps 4;

OY 10 SMKHHDDANVSMTFSN-----GK-LRVKGI---TYRNADICSRHRYTSAGLTQDLOL 58
DB 105 NWK-DESWIDVSNLKMWDYVVTGKLNKNGVDGFLDNLDVYSKYKXDSWFIQLN 162

RESULT 4

S31323

Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (*Pichia angusta*)

C:Species: *Pichia angusta*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000

C:Accession: S31323

R:Merckelbach, A.; Goedecke, S.; Janowicz, Z.A.; Hollenberg, C.P.

A:Description: Cloning and sequencing of the URA3 locus of the methylotrophic yeast *Hans*

A:Reference number: S31323

A:Accession: S31323

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-263 <MER>

A:Cross-references: EMBL:X69461; NID:92783; PIDN:CAAA221.1; PID:92784

C:Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylase

C:Keywords: carbon-carbon lyase; carboxy-lyase

F:3-263; Domain: orotidine-5'-phosphate decarboxylase homology <OPD>

Query Match

Best Local Similarity 17.0%; Score 63.5; DB 1; Length 263;
Matches 17; Conservative 7; Mismatches 12; Indels 7; Gaps 2;

OY 14 DQMANVSMTFSNGKLRVKGIYRN--ADICSRHRYTSAGL 53
DB 90 DRKFADIGNTV---KLYRGKGIYRTSKMADITNAHGVTGAGI 128

RESULT 5

F83476

Probable siderophore receptor PA1365 [Imported] - *Pseudomonas aeruginosa* (strain PA01)

C:Species: *Pseudomonas aeruginosa*

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83476

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V.

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83476

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-813 <STO>

A:Cross-references: GB:AE004565; GB:AE004091; NID:99947294; PIDN:AA04754.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1365

Query Match

Best Local Similarity 17.0%; Score 63.5; DB 2; Length 813;
Matches 19; Conservative 11; Mismatches 23; Indels 13; Gaps 3;

OY 6 TSLSSMKHDDANVSMTFSNGK-LRVKGI-----YYRNADICSRHRYT---SAG 52
DB 711 TAYLYKKPADNMNRLOATFFDSKDYRLDGVESFGRRQYSTTYVDLVSOYRTTPDDQLS 770

OY 53 LRLQDL 58
DB 771 LGIQNL 776

RESULT 6

T20881

hypothetical protein T25E12.4a - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000

C:Accession: T20881; T25282; T26254; T27354

R:Steward, C.

A:Description: submitted to the EMBL Data Library, March 1997

A:Reference number: Z19359

A:Accession: T20881

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <NTL>

A:Cross-references: EMBL:T292967; PIDN:CAB07478.1; GSPDB:GN00023; CESP:T25E12.4a

A:Experimental source: clone F14D1

R:Matthews, L.

A:Description: submitted to the EMBL Data Library, November 1996

A:Reference number: Z20009

A:Accession: T25282

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <MT2>

A:Cross-references: EMBL:T282052; PIDN:CAB04830.1; GSPDB:GN00023; CESP:T25E12.4a

A:Experimental source: clone T25E12

R:Barlow, K.

A:Description: submitted to the EMBL Data Library, January 1998

A:Reference number: Z20182

A:Accession: T26254

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <WI3>

A:Cross-references: EMBL:AL021572; PIDN:CAAI6519.1; GSPDB:GN00023; CESP:T25E12.4a

A:Experimental source: clone W06H3

R:Steward, C.

A:Description: submitted to the EMBL Data Library, January 1998

A:Reference number: Z20352

A:Accession: T27354

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <MI4>

A:Cross-references: EMBL:AL021507; PIDN:CAAI6430.1; GSPDB:GN00023; CESP:T25E12.4a

A:Experimental source: clone T70C5D

C:Genetics:

A:Gene: CBSP.T25E12.4a
 A:Map position: 5 77/1; 98/2; 201/1; 263/3; 310/1; 398/3; 440/3; 469/3; 506/1; 541/1; 571
 A:Insertions: 13/3; 77/1; 98/2; 201/1; 263/3; 310/1; 398/3; 440/3; 469/3; 506/1; 541/1; 571
 C:Superfamily: protein kinase C zinc-binding repeat homology <K2N1>
 F:322-371/Domain: protein kinase C zinc-binding repeat homology <K2N2>
 F:474-523/Domain: protein kinase C zinc-binding repeat homology <K2N2>

Query Match 16.4%; Score 61; DB 2; Length 1101;
 Best Local Similarity 30.9%; Pred. No. 53; Indels 12; Gaps 3;
 Matches 17; Conservative 11; Mismatches 15

OY 17 WANNVN-WFNSNGKLRKGIYVNDICSRHRTSA--GLTLDLQIMCNRIT 67
 DB 992 WKEISENIEFINGILOVK-----MSKRYVTYTKQSGIMQNTYLMSSDRLVL 1038

RESULT 7
 AC1866 hypothetical protein al10476 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AC1866
 R:Kanezo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, S.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabeta, S.; Nakazaki, N.; 205-213, 2001
 A:Title: Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC1866
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-274 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BAW72434.1; PID:g17129821; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al10476
 C:Superfamily: Synechocystis hypothetical protein slr2144

Query Match 16.1%; Score 60; DB 2; Length 274;
 Best Local Similarity 26.2%; Pred. No. 14; Indels 12; Gaps 2;
 Matches 16; Conservative 11; Mismatches 22

OY 4 HKHSLSSMKHD-----QDMANVSNKTSNGKLRKGIYVNDICSRHRTSAGTLTLD 57
 DB 109 YTTQLOSKMKEGNALIAETVNTITGSAGNNLAL-----NATIRSRQRTTGKISRQE 162
 OY 58 L 58
 DB 163 I 163

RESULT 8
 A12836 glycosyl hydrolase/lysozyme lyc [imported] - Agrobacterium tumefaciens (strain C58, Dupc
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: A12836
 R:Wood, D.W.; Setudal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClellan,
 science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: A12836
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-283 <KUR>
 A:Cross-references: GB:AE008668; PIDN:AA143111.1; PID:g17740583; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: lyc

A:Map position: circular chromosome

Query Match 16.1%; Score 60; DB 2; Length 283;
 Best Local Similarity 32.0%; Pred. No. 15; Indels 10; Gaps 3;
 Matches 16; Conservative 8; Mismatches 16

OY 1 HEAKTSLSSMKHDQDMANV--SNMTF-----SNCKLRK--GIYRNA 40
 DB 76 HEVHGIDVSKMNGVDWOTVRKSGSVFVFKATGSDRIDPKFGDHRSA 125

RESULT 9
 C97614 hypothetical 32.0k protein in Pfab-thid intergenic region [imported] - Agrobacterium

C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: C97614
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
 A:Title: Genome sequence of the plant pathogen and Biotechnology Agent Agrobacterium
 science 294, 2323-2328, 2001
 A:Reference number: A97359; PMID:11743194
 A:Accession: C97614
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK87868.1; PID:g15157256; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C.3846
 A:Map position: circular chromosome

Query Match 16.1%; Score 60; DB 2; Length 354;
 Best Local Similarity 32.0%; Pred. No. 19; Indels 10; Gaps 3;
 Matches 16; Conservative 8; Mismatches 16

OY 1 HEAKTSLSSMKHDQDMANV--SNMTF-----SNCKLRK--GIYRNA 40
 DB 147 HEVHGIDVSKMNGVDWOTVRKSGSVFVFKATGSDRIDPKFGDHRSA 196

RESULT 10
 S56421 Probable hexulose-6-phosphate synthase (EC 4.1.2.-) [similarity] - Escherichia coli (

N:Alternate names: hypothetical protein o216
 C:Species: Escherichia coli
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002
 C:Accession: S56421; G65230
 R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from
 A:Reference number: S56314; MUID:95334362; PMID:7610040
 A:Accession: S56421
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-216 <BUR>
 A:Cross-references: EMBL:U14003; NID:g1263172; PIDN:AA97092.1; PID:g537037
 A:Note: the nucleotide sequence was submitted to the EMBL data library, August 1994
 R:Blattner, F.R.; Mau, B.; Shao, Y.
 A:Title: The complete genome sequence of Escherichia coli K-12.
 science 277, 1453-1462, 1997

A:Reference number: A67420; MUID:97426617; PMID:9278503
 A:Accession: G65330
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-216 <BLAT>
 A:Cross-references: GB:AE000491; GB:U00096; NID:g2367357; PIDN:AACT7153.1; PID:g17906
 A:Experimental source: strain K-12, substrain MG1655

C:Genetics:
 A:Gene: yjiY
 C:Superfamily: hypothetical protein H1024
 C:Keywords: aldehyde-lyase; carbon-carbon lyase

1

T15023
hypothetical protein Y1108 - Yersinia pestis plasmid pMT1
C:Species: Yersinia pestis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T15023; T14697
R:Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A:Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
A:Reference number: Z18268; MID:99043898; PMID:9826348
A:Accession: T15023
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-187 <LIN>
A:Cross-references: EMBL:AF074611; NID:93883003; PID:93883106; PIDN:AAC82766.1
R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano,
submitted to the EMBL data Library, March 1998
A:Description: Structural organization of virulence determinants in three Yersinia pestis
A:Reference number: Z18168
A:Accession: T14697
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-187 <HUP>
A:Cross-references: EMBL:AF053947; NID:92996286; PID:92996333; PIDN:AAC13213.1
C:Genetics:
A:Gene: Y1108
A:Genome: plasmid pMT1
C:Superfamily: Yersinia pestis plasmid pMT1 hypothetical protein Y1108

Query Match 15.88; Score 59; DB 2; Length 187;
Best Local Similarity 37.18; Pred. No. 12;
Matches 13; Conservative 7; Mismatches 9; Indels 6; Gaps 1;

QY 16 DMANVSMTFSNGKLRVKGIVRRADICSRHRYTS 50
DB 124 DMADVAMWLEANGRLK-----ENAEIAHNAHYLS 152

Search completed: December 8, 2002, 19:34:47
Job time : 26.8129 secs

Tue Dec 10 10:51:45 2002

us-09-880-457-4_copy_20_87.ra1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 19:30:43 : Search time 14.4774 Seconds
(without alignments)
138.199 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAKRTSLSSMKHDDQWANY.....TSAGTLQLDLQMCNRIITH 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
4: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
5: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
6: /cgn2_6/prodata/1/aa/5B.COMB.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	47.7	317	US-08-996-139-13	Sequence 13, Appl
2	178	47.7	317	US-08-995-659-13	Sequence 13, Appl
3	178	47.7	317	US-09-215-649A-13	Sequence 4, Appl
4	178	47.7	317	US-09-052-521C-4	Sequence 13, Appl
5	178	47.7	317	US-09-577-780-13	Sequence 11, Appl
6	172	46.1	294	US-08-996-139-11	Sequence 11, Appl
7	172	46.1	294	US-09-215-649A-11	Sequence 11, Appl
8	172	46.1	294	US-09-577-780-11	Sequence 11, Appl
9	172	46.1	294	US-08-842-842-7	Sequence 2, Appl
10	172	46.1	316	US-08-989-362-2	Sequence 2, Appl
11	172	46.1	316	US-09-052-521C-2	Sequence 34, Appl
12	172	46.1	316	US-09-052-521C-34	Sequence 100, App
13	172	46.1	316	US-08-594-031-100	Sequence 102, App
14	172	46.1	316	US-08-594-031-102	Sequence 9, Appl
15	172	46.1	316	US-09-413-231-9	Sequence 33, Appl
16	172	46.1	316	US-09-052-521C-33	Sequence 93, Appl
17	172	46.1	316	US-08-332-562A-93	Sequence 6, Appl
18	172	46.1	316	US-08-618-911-6	Sequence 2, Appl
19	172	46.1	316	US-08-211-430-2	Sequence 1, Appl
20	172	46.1	316	US-08-761-136-1	Sequence 10, Appl
21	172	46.1	316	US-09-413-231-10	Sequence 20, Appl
22	172	46.1	316	US-08-472-240A-20	Sequence 12, Appl
23	172	46.1	316	US-09-257-490-12	Sequence 15, Appl
24	172	46.1	316	US-07-956-483-15	Sequence 75, Appl
25	172	46.1	316	PCT-US93-11703-75	
26	172	46.1	316		
27	172	46.1	316		

ALIGNMENTS

28	54	14.5	146	4	US-08-637-323-1	Sequence 1, Appl
29	54	14.5	149	3	US-08-584-031-16	Sequence 16, Appl
30	54	14.5	151	1	US-07-940-605A-3	Sequence 3, Appl
31	54	14.5	151	1	US-08-690-096-3	Sequence 2, Appl
32	54	14.5	261	1	US-07-940-605A-2	Sequence 8, Appl
33	54	14.5	261	1	US-08-184-422-8	Sequence 2, Appl
34	54	14.5	261	1	US-08-360-923A-2	Sequence 4, Appl
35	54	14.5	261	1	US-08-446-922-4	Sequence 4, Appl
36	54	14.5	261	2	US-08-431-055-4	Sequence 12, Appl
37	54	14.5	261	2	US-08-690-096-2	Sequence 12, Appl
38	54	14.5	261	2	US-08-249-189-12	Sequence 12, Appl
39	54	14.5	261	2	US-08-484-624A-12	Sequence 12, Appl
40	54	14.5	261	2	US-08-477-733B-12	Sequence 2, Appl
41	54	14.5	261	3	US-08-763-995-2	Sequence 12, Appl
42	54	14.5	261	3	US-09-088-913A-12	Sequence 8, Appl
43	54	14.5	261	3	US-08-589-771B-8	Sequence 12, Appl
44	54	14.5	261	4	US-08-769-819-12	Sequence 12, Appl
45	54	14.5	261	4	US-08-770-974-12	Sequence 12, Appl

RESULT 1
US-08-996-139-13
: Sequence 13, Application US/08996139
: Patent No. 6017729
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galiborff, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/996,139
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 317 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-996-139-13

Query Match 47.7% Score 178; DB 3; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSKRDHODMANNMTEFSGKLRV--GIYYRNADICSRHRTVSGLTQDLOL 60
Db 179 SHKVSLSWYHDKGMAKISNMTEFSGKLIYNODGYIYLANICFRHHTSGDLATEYLOL 238

RESULT 2

US-08-995-659-13
Sequence 13, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION NUMBER: US/08/995 659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-13

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSKRDHODMANNMTEFSGKLRV--GIYYRNADICSRHRTVSGLTQDLOL 60
Db 179 SHKVSLSWYHDKGMAKISNMTEFSGKLIYNODGYIYLANICFRHHTSGDLATEYLOL 238

RESULT 3
US-09-215-649A*13

Sequence 13, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSKRDHODMANNMTEFSGKLRV--GIYYRNADICSRHRTVSGLTQDLOL 60
Db 179 SHKVSLSWYHDKGMAKISNMTEFSGKLIYNODGYIYLANICFRHHTSGDLATEYLOL 238

RESULT 4

US-09-052-521C-4
Sequence 4, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:

APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Brv

CURRENT APPLICATION NUMBER: US/09/052,521C
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4

Tue Dec 19 10:51:45 2002

us-09-880-457-4_copy_20_87.ra1

Page 3

LENGTH: 317
TYPE: PRT
ORGANISM: Human
US-09-052-521C-4

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

3 AHKTSLSWKHDQWANSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLQDLOL 60
DB 179 SHKVSLSWYHDGKAKISNMTFSGKLRKLVNODGFYLIYANICFRHHTSGDGLATEYLQ 238

RESULT 5
US-09-577-780-13
Sequence 13, Application US/09577780
Patent No. 6419929

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0644
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

3 AHKTSLSWKHDQWANSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLQDLOL 60
DB 179 SHKVSLSWYHDGKAKISNMTFSGKLRKLVNODGFYLIYANICFRHHTSGDGLATEYLQ 238

RESULT 6

US-08-996-139-11
Sequence 11, Application US/08996139
Patent No. 6017729

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-996-139-11

Query Match 46.1% Score 172; DB 3; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDQWANSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLQDLOL 60
DB 156 SHKVSLSWYHDGKAKISNMTLSNGKLRKLVNODGFYLIYANICFRHHTSGSVFTDYLQ 215

RESULT 7
US-08-995-659-11
Sequence 11, Application US/08995659
Patent No. 6242213

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-995-659-11

Query Match 46.1% Score 172; DB 3; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDQWANSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLQDLOL 60
DB 156 SHKVSLSWYHDGKAKISNMTLSNGKLRKLVNODGFYLIYANICFRHHTSGSVFTDYLQ 215

RESULT 7
US-08-995-659-11
Sequence 11, Application US/08995659
Patent No. 6242213

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-995-659-11

Query Match 46.1% Score 172; DB 3; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDQWANSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLQDLOL 60
DB 156 SHKVSLSWYHDGKAKISNMTLSNGKLRKLVNODGFYLIYANICFRHHTSGSVFTDYLQ 215

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
TELEFAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-11

Query Match 46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 3 AHKTSLSWKHDQWVANSMTSNGKLRVK--GIYRNADICSRHRYVSAGLTLDLQ 60
DB 156 SHKVTLSWYHDKWAKISNMTLSNGKLRVNQDGFYLLVNICFRHHEISGSVPTDYLQ 215

RESULT 8
US-09-215-649A-11
Sequence 11, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
ZIP: 98101
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-215-649A-11

Query Match 46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 3 AHKTSLSWKHDQWVANSMTSNGKLRVK--GIYRNADICSRHRYVSAGLTLDLQ 60
DB 156 SHKVTLSWYHDKWAKISNMTLSNGKLRVNQDGFYLLVNICFRHHEISGSVPTDYLQ 215

RESULT 9
US-09-577-780-11
Sequence 11, Application US/095777780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
ZIP: 98101
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-577-780-11

Query Match 46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSMKRHDQDQMANVSNMTFSNGKLRVK--GIYRNADICSRHRTVSAGITLDDIQL 60
Db 156 SHKVTLSWYHDSGMKAKISNMTLSNGKLRVNDGFFYLLVNICFRHHETSGSVPTDYQL 215

RESULT 10
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-842-7

Query Match 46.1%; Score 172; DB 2; Length 316;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSMKRHDQDQMANVSNMTFSNGKLRVK--GIYRNADICSRHRTVSAGITLDDIQL 60
Db 178 SHKVTLSWYHDSGMKAKISNMTLSNGKLRVNDGFFYLLVNICFRHHETSGSVPTDYQL 237

RESULT 11
US-08-989-362-2
Sequence 2, Application US/08989362
Patent No. 6242586

GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: Mammalian Cell Surface Antigens: Related
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56

PRIOR APPLICATION DATA: US 60/032,846
APPLICATION NUMBER: 13-DEC-1996
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELEPHONE: (650)852-9196
TELEFAX: (650)456-1204

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-362-2

Query Match 46.1%; Score 172; DB 4; Length 316;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSMKRHDQDQMANVSNMTFSNGKLRVK--GIYRNADICSRHRTVSAGITLDDIQL 60
Db 178 SHKVTLSWYHDSGMKAKISNMTLSNGKLRVNDGFFYLLVNICFRHHETSGSVPTDYQL 237

RESULT 12
US-09-052-521C-2
Sequence 2, Application US/09052521C
Patent No. 6316408

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-4513rv
CURRENT FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-06-23
CURRENT APPLICATION NUMBER: 08/880,855
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patent Ver. 2.1

SEQ ID NO 2
LENGTH: 316
TYPE: PRT
ORGANISM: Mouse
US-09-052-521C-2

Query Match 46.1%; Score 172; DB 4; Length 316;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSMKRHDQDQMANVSNMTFSNGKLRVK--GIYRNADICSRHRTVSAGITLDDIQL 60
Db 178 SHKVTLSWYHDSGMKAKISNMTLSNGKLRVNDGFFYLLVNICFRHHETSGSVPTDYQL 237

RESULT 13

US-09-052-521C-34
; Sequence 34, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A45181V
; CURRENT APPLICATION NUMBER: US/09/052,521C
; PRIOR APPLICATION NUMBER: 1998-03-30
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 34
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-052-521C-34

Query Match
Best Local Similarity 19.3%; Score 72; DB 4; Length 28;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 3 AHKTSLSMKHDQMANVS 21
DB 9 SHKVTLSMWYHRCWAKIS 27

RESULT 14
US-08-594-031-100
; Sequence 100, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-594-031-100

Query Match
Best Local Similarity 16.9%; Score 63; DB 1; Length 376;
Matches 17; Conservative 16; Mismatches 28; Indels 16; Gaps 4;
QY 1 HEAKTSLS-SMKHDQMANVS---NMTESSG-----KLRVGIYRNADICSR 45
DB 189 HDHMYSTWYKSGDNTGISTHHTVNTVNGSTNTVRAAGCRSKTSGAGDNRDNCNR 248
QY 46 H-RVTSAGLTLDLQIM 61
DB 249 YGHNTTVGVNMTDVAMW 265

RESULT 15
US-08-594-031-102
; Sequence 102, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-594-031-102

Query Match
Best Local Similarity 16.9%; Score 63; DB 1; Length 376;
Matches 17; Conservative 16; Mismatches 28; Indels 16; Gaps 4;

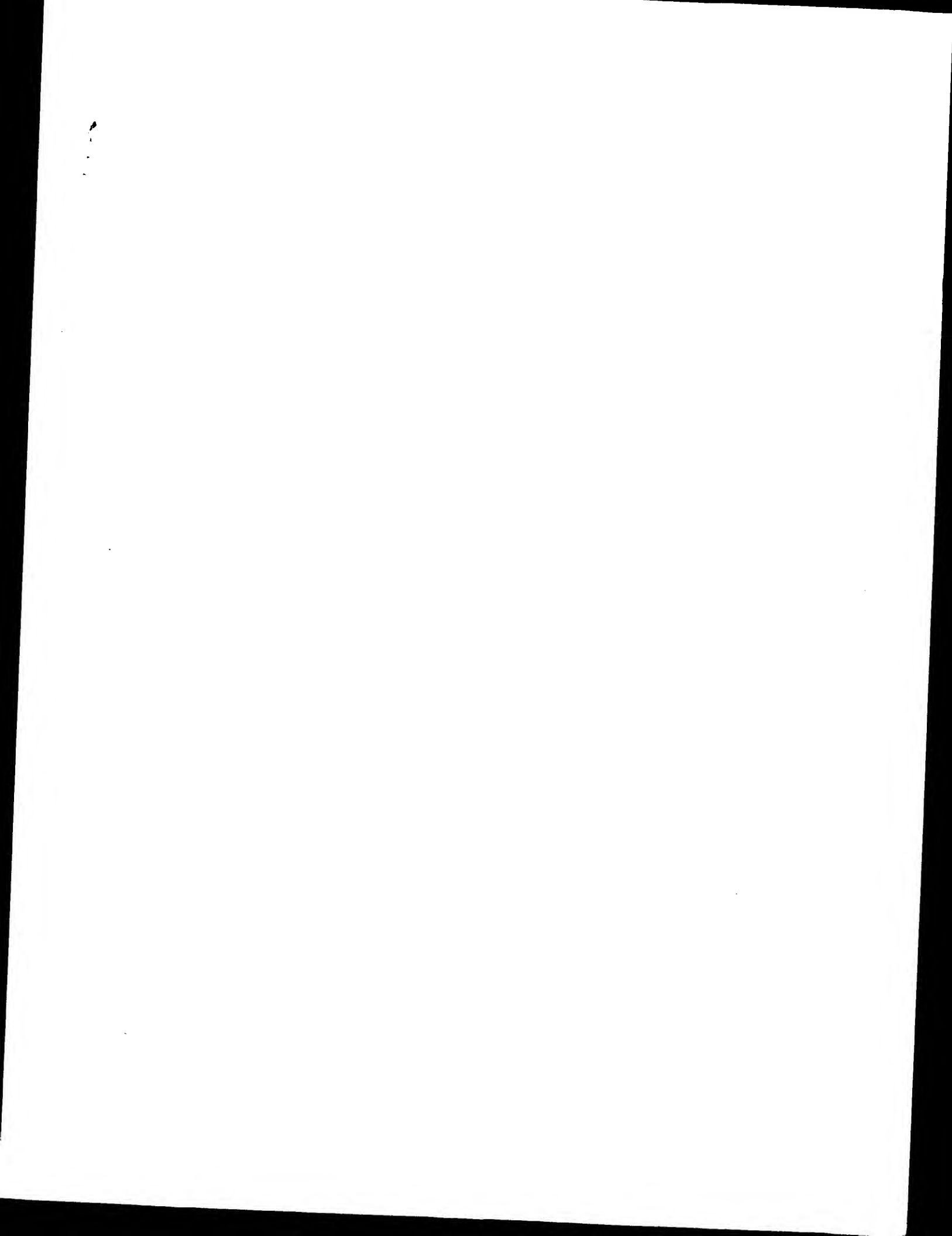
Tue Dec 10 10:51:45 2002

us-09-880-457-4_copy_20_87.raii

Page 7

```
OY      1 HEAAKTSLS-SWKHDQDWANYS---NNTFESG-----KLRYKGITYIRADICSR 45
          | | | | | : | | | | | : | | | | | : | | | | |
Db      189 HDSHNSITNYKKSGCNTGVSNHTVNTIYVNGTSTNYKAAGC RSKTS GAADNSRDNCNR 248
          | | | | | : | | | | | : | | | | | : | | | | |
OY      46 H-RVTSAGLLDLDLWL 61
          : | | | | : | | | |
Db      249 YGHATTVGVMNDIVMW 265
```

Search completed: December 8, 2002, 19:35:33
Job time : 16.4774 secs



Tue Dec 10 10:51:43 2002

us-09-880-457-4.ispt

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 8, 2002, 18:34:08 ; Search time 57.2516 Seconds
(without alignments)
313.111 Million cell updates/sec

Title: US-09-880-457-4
Perfect score: 1 MALLTSLQILLIPISRH.....TSAGITLQDLQMCNLRIRH 87
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mmc.*
9: sp-organelle.*
10: sp-phage.*
11: sp-plant.*
12: sp-rodent.*
13: sp-virus.*
14: sp-vertebrate.*
15: sp-unclassified.*
16: sp_rv.*
17: sp_bacteriap.*
18: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	69	15.2	214 13	Q9DDZ5
2	69	15.2	1130 15	Q88282
3	68.5	15.1	1171 17	Q97B77
4	68	14.9	107 10	Q9FGA8
5	67.5	14.8	491 4	Q9B561
6	67.5	14.8	491 4	Q9B561
7	67.5	14.8	491 4	Q9B561
8	67.5	14.8	1000 4	Q9B561
9	67.5	14.8	1018 4	Q9B561
10	67.5	14.8	1090 4	Q9B561
11	67.5	14.8	1214 4	Q9B561
12	67.5	14.7	296 16	Q9X2G7
13	67	14.7	307 10	Q9FT49
14	67	14.7	478 15	Q71146
15	67	14.7	1514 5	Q9NBK9
16	66.5	14.6		

17	66.5	14.6	1514 5	Q9VUN0
18	66	14.5	286 10	Q9C6R2
19	65.5	14.4	212 8	Q9G982
20	65	14.3	131 7	Q46867
21	65	14.3	210 10	Q49734
22	65	14.3	364 16	Q8RF50
23	65	14.3	621 10	Q9FMR6
24	64.5	14.2	276 16	Q9X6N2
25	64.5	14.2	355 17	Q97L30
26	64.5	14.2	355 17	Q97L30
27	64.5	14.2	427 16	Q9K9C9
28	64	14.1	1485 6	Q8NTM4
29	63.5	14.0	156 6	Q8S007
30	63.5	14.0	262 2	Q9FRC1
31	63.5	14.0	297 5	Q9VCF9
32	63.5	14.0	561 16	Q8YPE8
33	63.5	14.0	813 16	Q913X9
34	63	13.8	287 13	Q90WT9
35	63	13.8	345 16	Q8UIA0
36	62.5	13.7	156 6	Q8S008
37	62.5	13.7	246 8	Q8W109
38	62.5	13.7	251 10	Q942B1
39	62.5	13.7	336 3	Q9HDC3
40	62.5	13.7	439 3	Q9HDX9
41	62.5	13.7	2353 16	Q8XTZ4
42	62	13.6	158 17	Q96232
43	62	13.6	166 17	Q96232
44	62	13.6	638 10	Q9M393
45	62	13.6	774 5	Q9VJ73

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	214 AA.
Q9DDZ5	Q9DDZ5		
AC	Q9DDZ5		
PT	01-MAR-2001 (TREMUREL. 16, Created)		
DT	01-MAR-2001 (TREMUREL. 16, Last sequence update)		
DT	01-MAR-2002 (TREMUREL. 20, Last annotation update)		
DE	TRAIL-like protein.		
GN	Brachydanio rerio (zebrafish) (zebra danio).		
OS	Brachydanio rerio (zebrafish); Euteleostomi;		
OC	Euteleostomi; Metazoa; Chordata; Vertebrata; Osteichthyes; Cypriniformes;		
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	SEQUENCE FROM N.A.		
RA	Bobo J., Goetz F.W.,		
RT	"Molecular cloning and expression of a TNF receptor and two TNF		
RT	ligands in the fish ovary."		
RT	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).		
RU	EMBL, AF250041; AAG47640.1; -		
DR	HSSP, P50591; IDOG.		
DR	ZFIN, ZDB-GENE-010801-1; tnfrsf101.		
DR	InterPro, IPR003636; TNF_abc.		
DR	InterPro, IPR000478; TNF_family.		
DR	pfam, PF00228; TNF_1.		
DR	ProDom, PD002012; TNF_abc; 1.		
DR	SMART, SM00207; TNF_1.		
DR	PROSITE, PS50049; TNF_2; 1.		
DR	SEQUENCE 214 AA: 98C002474FF691AA CRC64:		
QY	Query Match	15.2%; Score 69; DB 13; Length 214;	
DB	Best Local Similarity	31.2%; Pred. No. 2.9;	
	Matches 15; Conservative 13; Mismatches 18; Indels 2; Gaps 1;		
	20 HEAKTSLSSWKHDDQANVSNFTPSNGKLRV--KGIYRNADICSRH 65		
	76 HOSCRHPTWANKSPGAHLNMTLNGRLRVFOGRTYLYISQVFRY 123		


```

DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01494; KVCHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR SMART: SM00225; BTB; 1.
KW Ionic channel.
FT VARIAM 450 A -> T.
SQ SEQUENCE 491 AA; 55970 MW; FFF12CA3CDA50185 CRC64;

Query Match
Best Local Similarity 22.0%; Score 67.5; DB 4; Length 491;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MATITSLQILLIPISHEAKTSLSS-----WKHDQMANVSNKTKRYKGIY 55
DB 328 LFLSVGISFVLYSVEKDHSSLSIPICMW-----WATISMTVGYG----- 374
QY 56 YRNADICSRHRTSAGITLQDLQMLNRII 86
DB 375 -----DTHPVTLAKGLIASTCIIGILV 398

RESULT 6
ID Q96B56 PRELIMINARY; PRT; 491 AA.
AC Q96B56;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Potassium voltage-gated channel, delayed-rectifier, subfamily S,
DE member 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015947; AAH15947.1.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
SQ SEQUENCE 491 AA; 56047 MW; 185D80646109C629 CRC64;

Query Match
Best Local Similarity 22.0%; Score 67.5; DB 4; Length 491;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MATITSLQILLIPISHEAKTSLSS-----WKHDQMANVSNKTKRYKGIY 55
DB 328 LFLSVGISFVLYSVEKDHSSLSIPICMW-----WATISMTVGYG----- 374
QY 56 YRNADICSRHRTSAGITLQDLQMLNRII 86
DB 375 -----DTHPVTLAKGLIASTCIIGILV 398

RESULT 7
ID Q9B031 PRELIMINARY; PRT; 491 AA.
AC Q9B031;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:4213) (Potassium voltage-gated channel,
DE delayed-rectifier, subfamily S, member 3).

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004987; AAH04987.1.
DR EMBL: BC004148; AAH04148.1.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003969; Kv6_channel.
DR InterPro: IPR003971; Kv9_channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR InterPro: IPR003974; Shaw_channel.
DR Pfam: PF00520; ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01492; KVCHANNEL.
DR PRINTS: PR01494; KVCHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01495; SHABCHANNEL.
DR PRINTS: PR01495; SHAWCHANNEL.
DR SMART: SM00225; BTB; 1.
SQ SEQUENCE 491 AA; 55984 MW; A5F12BF077A50DAD CRC64;

Query Match
Best Local Similarity 22.0%; Score 67.5; DB 4; Length 491;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MATITSLQILLIPISHEAKTSLSS-----WKHDQMANVSNKTKRYKGIY 55
DB 328 LFLSVGISFVLYSVEKDHSSLSIPICMW-----WATISMTVGYG----- 374
QY 56 YRNADICSRHRTSAGITLQDLQMLNRII 86
DB 375 -----DTHPVTLAKGLIASTCIIGILV 398

RESULT 8
ID Q9TT17 PRELIMINARY; PRT; 491 AA.
AC Q9TT17;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Voltage-gated delayed-rectifier potassium channel Kv9.3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=CORNEA ENDOTHELUM;
RA Rae J.L.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF209723; AAF22833.1.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003971; Kv9_channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.

```

DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01494; KY9CHANNEL.
DR PRINTS; PR01491; KY9CHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel
SQ SEQUENCE 491 AA; 55941 MW; 2EE396E0889D6F77 CRC64;

Query Match 14.8%; Score 67.5; DB 6; Length 491;
Best Local Similarity 22.0%; Pred. No. 12;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

OY 1 MAILTSQILLIPSTSHAKTSLS-----WKHDQWANSNMTEFNGKLRVAGIY 55
DB 328 LFLSVGISISVLTYSKDHSSLSLTPICWM-----WATISMTYVG----- 374
OY 56 YRMADICSRHRTSAGTLQDLQMCNLRIT 86
DB 375 -----DTHPVTLAKGLIASSTCIGCIIIV 398

RESULT 9

O9UIB9

AC 09UIB9; PRELIMINARY; PRT; 1000 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bicarbone transporter.
GN BT.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Romero M.F.;
RT "Cloning of a HCO3 transporter, NT2-NBC, from human brain, similar to
RT both the Anion exchangers (Aes) and the Na/Bicarbone cotransporters
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053755; AAF21720.1; -
DR HSSP; P02730; 1BNX.

DR InterPro; IPR001717; Anion-exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp. 1.
DR PRINTS; PR01231; HCO3TRANSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1000 AA; 112501 MW; 93FMA40A3141F8F7 CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 1000;
Best Local Similarity 31.9%; Pred. No. 27;
Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;

OY 16 PSISHEAKHTSLSSWKHDQMA-NVS--NMTEFNGKLRVAGIYRNADICSRHRTSAGL 72
DB 558 PNPSE-----TLQWKKNDITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
OY 73 TLQDLQMC 81
DB 606 YIPDVLEWC 614

RESULT 10

O60350

AC 060350; PRELIMINARY; PRT; 1018 AA.

DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sodium bicarbonate cotransporter2.
GN SBC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA TISSUE-RETINA;
RA Ishibashi K.; Sasaki S.; Marumo F.;
RT "Molecular cloning of a new sodium bicarbonate cotransporter cDNA from
RT human retina."
RL Biochem. Biophys. Res. Commun. 0:0-0(1998).
DR EMBL; AB012130; BAA25898.1; -
DR HSSP; P02730; 1BNX.

DR InterPro; IPR001717; Anion-exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp. 1.
DR PRINTS; PR01231; HCO3TRANSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
SQ SEQUENCE 1018 AA; 114204 MW; A3779D9D3A1E30BC CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 1018;
Best Local Similarity 31.9%; Pred. No. 28;
Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;

OY 16 PSISHEAKHTSLSSWKHDQMA-NVS--NMTEFNGKLRVAGIYRNADICSRHRTSAGL 72
DB 558 PNPSE-----TLQWKKNDITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
OY 73 TLQDLQMC 81
DB 606 YIPDVLEWC 614

RESULT 11

O9HC88

AC 09HC88; PRELIMINARY; PRT; 1090 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sodium bicarbonate cotransporter 2b.
GN NBC2b.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA TISSUE-KIDNEY;
RA Pushkin A.; Abduladze N.; Newman D.; Hwang J.; Kurtz I.;
RT "Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete
RT cds.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF089726; AAG16773.1; -
DR HSSP; P02730; 1BNX.
DR InterPro; IPR001717; Anion-exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp. 1.
DR PRINTS; PR01231; HCO3TRANSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1090 AA; 123080 MW; 541839C9B565896 CRC64;
Query Match 14.8%; Score 67.5; DB 4; Length 1090;
Best Local Similarity 31.9%; Pred. No. 30;
Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;

OY 16 PSISHEAKHTSLSSWKHDQMA-NVS--NMTEFNGKLRVAGIYRNADICSRHRTSAGL 72
DB 648 PNPSE-----TLQWKKNDITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 695
OY 73 TLQDLQMC 81
DB 696 YIPDVLEWC 704

```

Query Match          14.7%; Score 67; DB 16; Length 296;
Best Local Similarity 27.3%; Pred. No. 7.4; 19; Indels 10; Gaps 3;
Matches 15; Conservative 11; Mismatches 19;
QY      33 DODM--ANYSNMTEFSNGKLRYKRG--IYYRADICSRHRYTSAGITLQDIOLMC 81
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      244 EEDMEKFGVNPVFSDAMEIKGYIYYVGAADNC---IALATIPVEKYMKRC 294

RESULT 14
ID      09FT49 PRELIMINARY: PRT; 307 AA.
AC      09FT49;
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT      01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE      Hypothetical 34.9 kDa protein.
GN      T25B15.100.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      Spermatophyta; Magnoliophyta; euclcotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Alcaraz J.P., Clabault G., Cottet A., Maché R., Mewes H.W., Rudd S.,
RA      Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.;
RA      Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RL      [12]
RP      EU Arabidopsis sequencing project;
RA      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AL132972; CAC07924.1; -.
DR      Hypothetical protein.
KW      SEQUENCE 307 AA; 34863 MW; DC8746CB47D8F92E CRC64;
SQ

Query Match          14.7%; Score 67; DB 10; Length 307;
Best Local Similarity 18.3%; Pred. No. 7.8; 26; Indels 22; Gaps 2;
Matches 15; Conservative 19; Mismatches 26;
QY      20 HEAHTSLSSWKHDQM-----ANYSNMTFSNGKLRYKGIIYRN 58
       |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      149 HDKEYKLSFIWRNNKEVKRSEHHVLVCARTSMKKTCGHINHPYSOG-ITINGVLTYG 207

QY      59 ADICSRHYTSAGITLQDIOLMC 80
DB      208 AWTDKCYLMSPDLTSEDYGWV 229

RESULT 15
ID      071146 PRELIMINARY: PRT; 478 AA.
AC      071146;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      Envelope glycoprotein gp120 (Fragment).
EN      ENV.
GN      Human immunodeficiency virus type 1.
OS      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC      OC
OC      NCBI_TaxID=11676;
OX      [1]
RN      SEQUENCE FROM N.A.
RP      STRAIN=VE2;
RC      MEDLINE=96093896; PubMed=7576917;
RX      Quiñones-Mateu M.F., Dopazo J., Este J.A., Rota T.R., Domingo E.;
RA      "Molecular Characterization of human immunodeficiency virus type 1
RT      isolates from Venezuela."
RT      AIDS Res. Hum. Retroviruses 11:605-616(1995).
RL      [12]
RN      SEQUENCE FROM N.A.
RP      STRAIN=VE2;
RC
```

Query Match

Best Local Similarity	25.0%	score 6/;	DB 15;	Length 478;
Matches	21;	Conservative	13;	

Seq. ID	Seq. Name	Length	Score	E-value	Identity	Positives	Gaps
1	mslmatchnes	27	Indels	24	Gaps	3	

QY	21	EAHKTSLSSWKHDO	-----	DWANSNMTFSNGKLRVKGIYRNADIC	62
Db	74	OMHEDITSW-	----	OMHEDITSW-	----

0Y 63 SRHRYTSAGTIOPIOTNR-----EIKNC 127

Db 128 SENITTSGEKMOKEALFYNLDV 151

Search completed: December 8, 2002, 19:33:32
Job time : 68.2516 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model
December 8, 2002, 17:26:33 ; Search time 41.2387 Seconds
Run on: (without alignments)
310 722 Million cell updates/second

```

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAHTSLSSWKHDQWAV.....TSAGLTLDLQWLNCNLRHH 68

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
908470

```

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
                  Maximum Match 10
                  Listing first 45

```

Database :

A_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	358	96.0	95	23	AAU83632	Human PRO protein,
2	178	47.7	152	22	AAB67248	Human RANKL. Homo
3	178	47.7	160	21	AAB08273	Amino acid sequenc
4	178	47.7	244	23	AAU86148	Human PRO206 polyp
5	178	47.7	244	23	AAU78286	Human TRANCE prote
6	178	47.7	246	19	AAW83020	Osteoclastogenesis
7	178	47.7	317	19	AAW83195	Human osteoprotege
8	178	47.7	317	19	AAW83018	Osteoclastogenesis
9	178	47.7	317	19	AAW69577	Human osteoprotege
10	178	47.7	317	19	AAW69577	NF-kB receptor act
					AAW68293	NF-kB receptor act

11	178	47.7	317	21	AAV84417	Amino acid sequenc
12	178	47.7	317	22	AAE08738	Amino receptor act
13	178	47.7	317	22	AAE04426	Human receptor act
14	178	47.7	317	22	AAE01993	Human full-length
15	178	47.7	317	23	AAE08134	Human RANKL polype
16	178	47.7	317	23	AAV78285	Human TRANCE prote
17	177	47.5	318	22	AAU08386	Mouse FLAG-murine
18	175	46.9	318	22	AAU082092	Rat osteoclast dif
19	175	46.6	318	22	AAV17873	Human TRANCE. Hom
20	172	46.1	160	21	AAV91023	Mouse OBM protein
21	172	46.1	173	21	AAV84421	Amino acid sequenc
22	172	46.1	173	21	AAV84425	Amino acid sequenc
23	172	46.1	182	21	AAV84442	DNA encoding osteo
24	172	46.1	182	21	AAV84430	Amn osteoprotegerin
25	172	46.1	187	21	AAV84433	Amn osteoprotegerin
26	172	46.1	188	21	AAV83019	A murine OCIF-bind
27	172	46.1	244	19	AAW69356	NF-kB receptor act
28	172	46.1	294	19	AAW68292	NF-kB receptor act
29	172	46.1	294	22	AAE08737	Murine receptor ac
30	172	46.1	294	22	AAE04425	Murine receptor ac
31	172	46.1	324	22	AAE01992	Murine RANKL (rece
32	172	46.1	324	22	AAE01992	Human osteoprotege
33	172	46.1	316	19	AAW83194	Osteoclastogenesis
34	172	46.1	316	19	AAW59654	Amino acid sequenc
35	172	46.1	316	20	AAV17874	Murine TRANCE. Mu
36	172	46.1	316	21	AAV91024	Murine OBM protein
37	172	46.1	316	21	AAV84418	Amino acid sequenc
38	172	46.1	316	21	AAV84419	Amino acid sequenc
39	172	46.1	316	23	AAV78289	Mouse TRANCE prote
40	172	46.1	409	23	AAV01715	GlutathioneStransf
41	172	46.1	409	23	AAV97111	Murine GSR-mDGF fu
42	172	46.1	501	22	AAW84420	Amino acid sequenc
43	172	46.1	501	21	AAV84422	A murine osteoprot
44	162	43.4	173	21	AAV84426	Am osteoprotegerin
45	145	38.9	173	21		

ALIGNMENTS

RESULT	1
AAU83632	
ID	AAU83632 standard; Protein; 95 AA.
XX	
AC	AAU83632;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human PRO protein, Seq ID No 82.
XX	
KW	Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
KW	
OS	Homo sapiens.
XX	
PN	WO20020828-A2.
XX	
PD	31-JAN-2002.
XX	
PE	29-JUN-2001; 2001MO-US21066.
XX	
PR	20-JUL-2000; 2000US-219556P.
PR	25-JUL-2000; 2000US-220585P.
PR	25-JUL-2000; 2000US-220607P.
PR	25-JUL-2000; 2000US-220624P.
PR	25-JUL-2000; 2000US-220638P.
PR	25-JUL-2000; 2000US-220664P.
PR	25-JUL-2000; 2000US-220666P.
PR	25-JUL-2000; 2000US-220893P.
PR	28-JUL-2000; 2000MO-US20710.

PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-0000009.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2000WO-US34956.
 PR 10-MAY-2001; 2001US-0506520.
 PR 25-MAY-2001; 2001US-0854280.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Garney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 DR WPI: 2002-172001/22.
 DR N-PSTB; ABK3576.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT tumour or liver tumour -
 XX
 PS Claim 11; Figure 82; 359pp; English.
 CC
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumours, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for stimulating
 CC for stimulating the release of tumour necrosis factor-alpha from human blood,
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.
 XX
 SO Sequence 95 AA;
 Query Match
 Best Local Similarity 96.0%; Score 358; DB 23; Length 95;
 Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 HEAHTSLSSMKHDQDWMANVSNMFTSNGKLRVKGITYRNADICSHRYTSAGLTLDLQL 60
 DB 20 HEAHTSLSSMKHDQDWMANVSNMFTSNGKLRVKGITYRNADICSHRYTSAGLTLDLQL 79
 OY 61 WCNLRIT 67
 DB 80 WCNLRISV 86
 RESULT 2
 AAB67248
 ID AAB67248 standard; protein: 152 AA.
 AC AAB67248;
 XX
 DT 18-APR-2001 (first entry)
 DE Human RANKL.
 XX
 KM Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
 OS Homo sapiens.
 XX

PN WO200100832-A1.
 XX
 PD 04-JAN-2001.
 PF 26-JUN-2000; 2000WO-US17579.
 PR 28-JUN-1999; 99US-0141342.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
 PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
 DR WPI: 2001-123012/13.
 XX
 PT Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications -
 XX
 PS Disclosure; Fig 3; 60pp; English.
 CC
 CC The present invention relates to a formulation comprising Apo-2
 CC ligand and divalent metal ions. Apo-2 ligand and the formulation
 CC of divalent metal ions for making Apo-2 ligand and formulations
 CC containing Apo-2 ligand results in increased yield and stability
 CC of Apo-2 ligand trimers.
 XX
 SO Sequence 152 AA;
 Query Match
 Best Local Similarity 47.7%; Score 178; DB 22; Length 152;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
 OY 3 AHTSLSSMKHDQDWMANVSNMFTSNGKLRVKGITYRNADICSHRYTSAGLTLDLQL 60
 DB 17 SHRYTSAGLTLDLQL 60
 RESULT 3
 AAB08273
 ID AAB08273 standard; protein: 160 AA.
 AC AAB08273;
 XX
 DT 04-DEC-2000 (first entry)
 DE Amino acid sequence of a human TNF ligand QPGL.
 XX
 KM ACP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KM type II transmembrane protein; B cell stimulatory factor;
 KM inflammatory disorder; immune disorder; rheumatoid arthritis;
 KM lupus and graft versus host disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200047740-A2.
 PD 17-AUG-2000.
 PF 11-FEB-2000; 2000WO-US03653.
 PR 12-FEB-1999; 99US-0119906.
 PR 18-NOV-1999; 99US-0166271.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Hsu H;
 DR WPI: 2000-558217/51.
 PT Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.

PT	rheumatoid arthritis -
XX	
PS	Claim 14; Fig 9; 71pp; English

Query Match	47.7%	Score 178;	DB 21;	length 160;	
Best Local Similarity	60.0%	Pred. No. 2,4e-15;			
Matches 36;	Conservative	5;	Mismatches 17;	Indels 2;	Gaps 1

Db 22 SHKVSLSSTWINDPQNNHSTSS
RESULT 4
AAU06148
ID AU186148 standard; protein; 244 AA

LD	AAU8614B;	
XX	15-JUL-2002	(first entry)
AC		
XX		
DT		
XX		
DE	Human	PRO206 polypeptide.
XX		
XX	Human; PRO;	benign tumour; malignant tumour; lymphoid malignancy;
KM	leukaemia;	neutroal disorder; stromal disorder; blastocoealic disorder;
KM	inflammatory disorder;	immune disorder; angiogenic disorder;
KM	cytostatic;	neuroprotective.

XX	Homo sapiens.
OS	
XX	
PN	W0200153486-A1

XX	26-JUL-2001.
PD	
XX	
PF	11-FEB-2000; 2000WO-US03565

XX	08-MAR-1999;	99WO-US05028
PR	11-MAR-1999;	99US-123972P
PR	11-MAY-1999;	99US-133459P
PR	02-JUN-1999;	99WO-US12252

PR 26-JUN-1999; 99US-140650P
PR 22-JUN-1999; 99US-140653P
PR 20-JUL-1999; 99US-144578P
PR 26-JUL-1999; 99US-145688P
PR 26-JUL-1999; 99US-146222P

PR 28-JUL-1999; 9905-149395B
PR 17-AUG-1999; 9905-151689J
PR 31-AUG-1999; 99WO-US20111
PR 01-SEP-1999; 99WO-US21091
PR 15-SEP-1999; 99WO-US20319

PR	30-NOV-1999;	99WO-US2830
PR	01-DEC-1999;	99WO-US2830
PR	01-DEC-1999;	99WO-US2863
PR	05-JAN-2000;	2000WO-US0021

AA (GETH) GENENTECH INC. Hillan KJ
PA
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Stone DM;
PI Marsters SA, Pan J, Pitter RM, Roy MB, Smith V,
PI

PI	Watanabe CK, Wood WI
XX	WPI; 2002-205567/26.
DR	N-PSDB; ABK40274.
DR	

xx Thirty-five nucleic acids encoding Pro, Phe, Arg, Gly, Ser, Thr, Asn, Gln, Asp, Glu, Lys, Ile, Val, Leu, and Tyr
 pt Treating benign or malignant tumors, leukemias and lymphoid
 pt malignancies, inflammatory, angiogenic and immunologic disorders
 xx
 Claim 61; Fig 42; 302pp; English.
 ps

XX The present invention relates to the isolation of novel human
CC polypeptides and the polynucleotide sequences encoding them. The
CC polypeptides and the polynucleotide sequences encoding them are
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular
CC macrophagal, stromal and blastocoelel disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. AA086128-AA086162 represent the human PRO
CC polypeptides of the invention.
XX

Sequence	244 AA;	Score 178;	DB 23;	Length 244;
Query Match		47.7%;		
Best Local Similarity		Pred. No. 4.1e-15;		
Matches	36; Conservative	5; Mismatches	17; Indels	2; Gaps

	AHKTSLSSWKHDODMANVSNMTEFNSNGRLAV		:	: :					:	:
OY	:: :: :	:	:	:	:	:	:	:	:	:
Dd	SHKVSLSWYHDRGMAKISNMTEFSNGLIVNOGFIYLXANICFRHHETSGIATEFYQL									165

RESULT 5
AAU78286
ID AAU78286 standard; Protein; 244 AA

XX	AAU78286;
AC	
XX	18-JUN-2002 (first entry)
DT	
XX	

AA	Human TRANCE protein splice variant 2
DE	
XX	tumour necrosis factor-related
KW	dwarfism; osteopetrosis; cran-
KW	iochondroplasia damage; trauma

KW	bone damage; cartilage	gigantism; exostosis; chondrocyte
KW	rheumatoid arthritis; acromegaly	exostosis; chondrocyte
KW	exostosis bursata; multiple osteocartilaginous	exostosis; chondrocyte
KW	cartilage growth; skeletal growth.	
XY		

AA	Homo sapiens.
OS	
XX	W0200216551-A2.
PN	
XX	

PD	28-FEB-2002.
XX	20-AUG-2001; 2001WC-US26101
PF	
XX	18-AUG-2000; 2000US-226197H
PR	

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
PA
XX
XX Choi Y, Odgren PR, Marks SC;
PI
XX

AA	WPI; 2002-304119/34.
DR	N-PSDB; ABK12877.
DR	
XX	Treating mammal have
PT	

PT cartilage/synovial tissue, joint
PT administering tumour necrosis factor-related activation-inducing ligand to mammal -
PT cytokine-modulating agent to mammal -
XX
PS Disclosure; Fig 4; 55pp; English.

XX The present invention relates to a new method of treating a mammal
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth. The method of the invention involves administering to
 CC the mammal a tumour necrosis factor-related activation induced cytokine
 CC (TRANCE)-modulating agent. The method is useful for treating a cytokine
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth, where the disorder comprising insufficient cartilage or
 CC craniofacial growth is selected from dwarfism, osteopetrosis,
 CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
 CC arthritis, and disorders comprising excessive cartilage or skeletal
 CC growth are selected from acromegaly, gigantism, exostosis, carpal tunnel
 CC exostosis, bursitis and multiple osteocartilaginous exostoses. The method
 CC is useful for inhibiting chondrocyte differentiation. The present amino
 CC acid sequence represents the human TRANCE protein, splice variant 2, of
 CC the invention. TRANCE is a member of the tumour necrosis factor family
 CC and acts directly on cartilage-producing cells (chondrocytes).

SO Sequence 244 AA;

Query Match

Best Local Similarity 47.7%; Score 178; DB 23; Length 244;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHDDMANVSNMTFSNGKLRVK--GIYRNADICSRHRYVSAGLTLDL 60
 Db 106 SHKVSLSWYHDKGMAKISNMTFSNGKLIYNQDGFYLVANICFRHETSGDLATEYLD 165

RESULT 6

AAW83020
 ID AAW83020 standard; Protein: 246 AA.

AC AAW83020;

DT 10-FEB-1999 (first entry)

DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 KW Osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 human.

OS Homo sapiens.

PN WO984644-A1.

PD 22-OCT-1998.

PF 15-APR-1998; 98WO-JP01728.

PR 02-DEC-1997; 97JP-033241.

PR 15-APR-1997; 97JP-0097808.

PR 09-JUN-1997; 97JP-0151434.

PR 12-AUG-1997; 97JP-0217897.

PR 21-AUG-1997; 97JP-0224803.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morioka T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;

DR WPI: 1998-594563/50.

DR N-PSDB; AAV69899.

PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism

PS Example 28; Pages 119-120; 151pp; Japanese.

XX

CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone.
 CC Absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC affinity factor by separation and solubilisation of membrane proteins
 CC used for screening potential inhibitors and modulators of its biological
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC active, and screening for receptors to OBM which mediate its biological
 CC function and calcium metabolism. The antibodies can be used for assay
 CC components of drugs.

SO Sequence 246 AA;

Query Match

Best Local Similarity 47.7%; Score 178; DB 19; Length 246;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHDDMANVSNMTFSNGKLRVK--GIYRNADICSRHRYVSAGLTLDL 60
 Db 108 SHKVSLSWYHDKGMAKISNMTFSNGKLIYNQDGFYLVANICFRHETSGDLATEYLD 167

RESULT 7

AAW83195
 ID AAW83195 standard; Protein: 317 AA.

AC AAW83195;

DT 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the pcDNA/huOPBP1.Insert.
 KW Osteoporosis; osteoclast maturation; bone disease; metastasis; ODAK;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease.

OS Homo sapiens.

PN WO9846751-A1.

PD 22-OCT-1998.

PF 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880835.

PA (AMGE-) AMGEN INC.

PI Boyle WJ;

DR WPI: 1998-594578/50.

DR N-PSDB; AAV70285.

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis

PS Claim 19; Fig 4; 47pp; English.

CC The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for

CC Characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

SO Sequence 317 AA;

Query Match 47.7%; Score 178; DB 19; Length 317;
 Best Local Similarity 60.0%; Pred. No. 5.8e-15;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHDQWAVNSNMTFSGKLRVK--GIYRNADICSRHRTYAGTLQDQL 60
 Db 179 SHKYSLSWYHGRGWAKISNMTFSGKLIYNQDGFYLYANICFRHHTSGDLATEYIQL 238

RESULT 10

AAW68293
 ID AAW68293 standard; Protein; 317 AA.

AC AAW68293;

DT 08-OCT-1998 (first entry)

DE NF-kB receptor activator RANK ligand (RANKL).

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF.

OS Homo sapiens.

PN WO9828424-A2.

PD 02-JUL-1998.

PE 22-DEC-1997; 97WO-0523866.

PF 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

PA (IMMUNEX CORP.

PI Anderson DM, Galibert LJ, Maraskovsky E;

DR WPI: 1998-377655/32.

DR N-PSDB; AAW41372.

PS New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis
 PS Example 7; Pages 59-60; 80pp; English.

CC This represents a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

SO Sequence 317 AA;

Query Match 47.7%; Score 178; DB 19; Length 317;
 Best Local Similarity 60.0%; Pred. No. 5.8e-15;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHDQWAVNSNMTFSGKLRVK--GIYRNADICSRHRTYAGTLQDQL 60
 Db 179 SHKYSLSWYHGRGWAKISNMTFSGKLIYNQDGFYLYANICFRHHTSGDLATEYIQL 238

RESULT 11

AAW84417
 ID AAW84417 standard; Protein; 317 AA.

AC AAW84417;

DT 25-JUL-2000 (first entry)

DE Amino acid sequence of a human osteoprotegerin ligand (OPGL).

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.

OS Homo sapiens.

PN Key Location/Qualifiers

FT Region 49..69

FT Domain /note= "transmembrane region"

FT Region /note= "extracellular stalk domain"

FT Region /note= "active ligand moiety"

PN WO200015807-A1.

PD 23-MAR-2000.

PF 13-SEP-1999; 99WO-DK00481.

PR 15-SEP-1998; 98DK-0001164.

PR 02-OCT-1998; 98US-0102896.

PA (MEBT-) M & E BIOTECH AS.

PI Halkier T, Haaning J;

DR WPI: 2000-271444/23.

DR N-PSDB; AA29964.

PS In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -
 PT Claim 19; Page 78-79; 110pp; English.

CC The present sequence represents a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.

SO Sequence 317 AA;

transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjuvant therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating osteoclast function and activities. They are useful for modulating osteoclast function with excess bone resorption precursors and for modulating osteoclast activity. The RANK DNAs are used as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, while the proteins are useful for the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is RANK ligand (RANKL) protein from human.

Sequence 317 AA:

Query Match 47.7%; Score 178; DB 22; Length 317;
Best Local Similarity 60.0%; Pred. No. 5..8e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

Oy 3 AKHTSISSWKHDQWVANSNTEFNCKLRK--GIYRNADICSRHRVTSGILTDLDL 60
 :||| ||||| |:: ::||| ||||| | | | | | | | | | | | |
Db 179 SHKVSLSMYHIDRGWAKISNTFESNGKLIVNQDGFYLTVANICFRHHETSDGLATEHYDL 238

RESULT 13
AAE04426 standard; Protein: 317 AA.
XX AAE04426;
AC AAE04426;
DT 04-SEP-2001 (first entry)
DE Human receptor activator of NF-chi B ligand (huRANKL) protein.
DD Human receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF
DX XX Human; receptor activator of NF-chi B; RANK; immune response;
KW CD40; TNF receptor-associated factor; TRAF; ligand; transmembrane protein.
RW chromosome 18q22.1; huRANKL; chromosome 13q14;
KM chromosome 18q22.1; huRANKL; chromosome 13q14;
KV Homo sapiens.
OS
XX Key Location/Qualifiers
FH 162..317
FT Region /note="Receptor binding region"
FI
FN
PN US6242213-B1.
PD 05-JUN-2001.
PZ 97US-0995659.
PF 22-DEC-1997;
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
PA (IMMUNE) IMMUNEX CORP.
PI Anderson DM;
DR WPT_2001-407216/43.
DIR N-PSTDB; AAD08715.
XX New DNA molecules, useful for producing ligands (which are useful for
PT regulating immune response and in screening for inhibitors of NF-chi B
PT receptor activator) of the receptor activator of NF-chi B (RANK) -
PS Claim 1: Column 65-66; 43pp. English.
CC The present invention relates to receptor activator of NF-chi B (RANK) to
CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC proteins respectively. RANK is a member of the tumour necrosis factor
CC (TNF) superfamily and it closely resembles CD40 in the extracellular

CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC present amino acid sequence is full-length human RANL1 (huRANL1).
CC protein. The RANL1 gene is located in chromosome 13q14.
XX
XX

Query Match	47.7%	Score 178;	DB 22;	Length 317.
Best Local Similarity	60.0%			

Conservative	Mismatches	Indels	Gaps
30	5	17	2

3 AHKISLSSAKHDQDMANVSNMTFSNCKLRVK-GIYYRMADICSRIHVTSGATLDDQL 60
179 SHKYSLSSTWYHDKGWAKISNMTFSNCKLYINQDGFYLLYANICFRHHTSGDT

RESULT	15
ABB08134	
ID	ABB08134
standard; protein:	317

ABB08134;

Human RANKL polypeptide.

M dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
W fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
S tuberculostatic; cytostatic; human; RANKL.
X Homo sapiens.
X
X WO200236141-A2.

10-MAY-2002.

30-OCT-2001;

02-NOV-2000; 2000US-245731b

(IMMV) IMMUNEX CORP.

Lynch DH, De Smedt TR
Thomas FK.

WPI: 3003 F00111

Treating an individu

chickenpox or AIDS, by administering a combination of dendritic mobilization factor or matured dendritic cells.

antigen-specific T cells - maturation agent, T cell enhancing factor and

The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism. The method involves administering a pathogenic or opportunistic organism. The method agent: (a) dendritic cell mobilization factor; (b) dendritic cells comprising: (c) dendritic cell mobilization factor; (d) dendritic cell maturation agent; (e) activated, antigen-specific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria (e.g. *M. tuberculosis*), yeast, fungi (e.g. *C. albicans*) or protozoa (e.g. *T. cruzi*), which causes Chagas disease). The antibodies are especially useful for treating an individual suffering from immunosuppression by enhancing a lymphocyte-mediated immune response. In particular, the method is useful for treating inflammation, chickenpox, oral or genital herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T cell leukemia or T cell lymphoma. The activated antigen-presenting dendritic cells are useful as a vaccine adjuvant. The present sequence represents a human RANKL polypeptide fragment.

1
2
3
4

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 8, 2002, 17:28:38 ; Search time 16.2774 Seconds
(without alignments)
221.684 Million cell updates/sec

Title: US-09-880-457-4

perfect score: 455

Sequence: 1 MATLTLSDLLILLIPISH.....TSAGITLDDLMCNLRITIH 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	180.5	39.7	317 1	TN11_HUMAN
2	177.5	39.0	318 1	TN11_HUMAN
3	176	38.7	316 1	TN11_MOUSE
4	78.5	17.3	501 1	CSU2_DROME
5	66	14.5	310 1	SC65_YARLI
6	65.5	14.4	641 1	NU5M_ALIMA
7	64	14.3	251 1	Y108_CHLTA
8	63.5	14.1	334 1	GUB_CLOTM
9	63.5	14.0	263 1	PYRE_PICAN
10	63	13.8	119 1	YRAN_HAEIN
11	61.5	13.5	269 1	IL1B_HRIU
12	61.5	13.5	329 1	IPNS_STRCL
13	61.5	13.5	1078 1	CVAY_BOVIN
14	61	13.4	851 1	NUD1_YEAST
15	61	13.4	2144 1	GUT1_YEAST
16	60.5	13.3	1451 1	SPT6_YEAST
17	60	13.2	196 1	TRAP_ECOLI
18	60	13.2	301 1	Y186_MYCPN
19	59.5	13.1	783 1	APE2_SULSO
20	59.5	13.1	216 1	SCAH_ECOLI
21	59.5	13.1	329 1	IPNS_STRU
22	59.5	13.0	561 1	ATKA_ANAST
23	58.5	12.9	958 1	AMYG_DEBHC
24	58.5	12.9	1859 1	GBFL_HUMAN
25	58.5	12.9	551 1	FIXN_AZOC
26	58	12.7	478 1	DISR_AGRH
27	57.5	12.6	525 1	ATPL_YEAST
28	57.5	12.6	532 1	GSNC_PEA
29	57.5	12.6	677 1	RNL4_YEAST
30	57.5	12.6	1856 1	GBFL_CRIGR
31	57.5	12.6	2156 1	RPL_HUMAN
32	57.5	12.6	72 1	COR2_DROME
33	57	12.5		

34	57	12.5	720 1	KRE6_YEAST
35	57	12.5	1444 1	KRPL_RDYP
36	57	12.5	1585 1	P3K3_DICDI
37	56.5	12.4	158 1	2SS_SOYBN
38	56.5	12.4	161 1	VP7_BPPH
39	56.5	12.4	286 1	TEHB_HAEIN
40	56.5	12.4	333 1	IPNS_STRLP
41	56.5	12.4	404 1	FCGL_MOUSE
42	56.5	12.4	404 1	ISCS_METTE
43	56.5	12.4	544 1	ISCS_SOYBN
44	56.5	12.4	550 1	YSRL_CAREL
45	56.5	12.4	587 1	ULB4_HCMVT

ALIGNMENTS

RESULT 1
ID TN11_HUMAN STANDARD: PRT: 317 AA.
AC 014788: 014723: Q9P203: Q96Q17;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCB1; Taxid:9606;
OX [1]
RN .SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE-Bone marrow, and Periphera blood;
RC MEDLINE-98032977; PubMed-9367155;
RX Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RN .SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE-Lymph node;
RC MEDLINE-98227661; PubMed-9568710;
RX Tacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Sullivan S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RN .SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RP Ikeda T., Kuroyama H., Hirokawa K.,
RA "Determination of human RANKL isoforms.";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN .SEQUENCE OF 73-317 FROM N.A.
RP TISSUE-Thymocytes;
RC MEDLINE-97460112; PubMed-9312132;
RX Wong B.R., Rho J., Aron J., Robinson E., Orlicki J., Chao M., Lee S.Y.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [5]
RN .SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE-Tongue;

RX MEDLINE-20175237; PubMed-10708588;
RA Nagai M., Kyakumoto S., Sato N.;
RT "Cancer cells responsible for humoral hypercalcemia express mRNA
RT encoding a secreted form of ODF/TNFRANK that induces osteoclast
RL formation.";
CC Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC secreted (isoform 2). A soluble form of isoform 1 arises by
CC proteolytic processing (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing (By similarity). The cleavage may be
CC catalyzed by ADAM17.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF019047; AAB86811.1; -
DR EMBL: AF053712; AAC39731.1; -
DR EMBL: AB064269; BAB79694.1; -
DR EMBL: AB061227; BAB71768.1; -
DR EMBL: AB064270; BAB79695.1; -
DR EMBL: AF013171; AAC51762.1; -
DR HSSP: AB037599; BAA90488.1; -
DR HSSP: P50591; ID06; -
DR Gene: HGNC:11926; TNFSF11.
DR MIM: 602642; -
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR PROSITE: PS00049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing.
FT CHAIN 1 317
FT DOMAIN 140 317
FT TRANSMEM 48 68
FT DOMAIN 69 317
FT SITE 139 140
FT CARBOHYD 171 171
FT VARSPLIC 198 198
FT VARSPLIC 1 47
FT CONFLICT 1 73
FT CONFLICT 194 194
FT SEQUENCE 317 AA: 35478 MW: 7661764463480976 CRC64;
Query Match 39.7%; Score 180.5; DB 1; Length 317;

Best Local Similarity 59.7%; Pred. No. 1.3e-13;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
OY 15 IPSTSHRHTSSLSMKHDDMANVSNMTFSNGKLVK--GIYRNADICSHRYTSAGL 72
Db 175 IPGSGS---HKVSLSSWYHDKGMKISMFTFSNGKLVNDGTYLYLVANICFRHHTSGDL 231
OY 73 TLQDLDL 79
Db 232 ATETYLQ 238
RESULT 2
TNI1_RAT
AC O9ESE2; 091219; STANDARD; PRT; 318 AA.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TNF) (osteoprotegerin ligand) (OPGL) (osteoclast
DE TNFSF11 OR RANKL OR TNF) (ODF).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP [1]
RC TISSUE=Tibial bone;
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
RN [2]
RP SEQUENCE OF 266-318 FROM N.A.
RC STRAIN=Fischer 344;
RX PubMed=11804028;
RA Olgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savvas A.,
RA Safadi F.F., Popoff S.N., Lengner C., van-Hol W., Choi Y.,
RA Marks S.C. Jr.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the TNFSF11 (TNF, RANKL, ODF, OPGL) gene.";
RL Int. J. Dev. Biol. 45:853-859(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF187319; AAG17031.1; -
DR EMBL: AF425669; AAL23963.1; -

RL Nature 390:175-179(1991)

Query Match		Pred. No. 3e-13	5	Gaps	2
Best Local Similarity	58.2%				
Matches	39; Conservative	4; Mismatches	19; Indels		

```

RESULT 3
TN11_MOUSE
SOURCE
STANDARD;
PRT; 316 AA
END

```

RA Nature 367:109-118 (1994).
RN [13] SEQUENCE FROM N.A. (ISOFORM 1).
RN
RP TISSUE-BONE marrow:
RC MEDLINE=96221661; PubMed=9568710; Kelley M.J., Dunstan C.R., Hsu H.,
RX Lacey D.L., Timms E., Tan H.-L., Colombero A., Elliott G., Scully S., Rasmussen J.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Eli A., Qian Y.-X., Sullivan J., Hawkins N., Davy E., Capprelli C., Guo J., Delaney J., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Boye W.J.; "osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation." Cell 93:165-176(1998).
RL [14] SEQUENCE FROM N.A. (ISOFORM 1).
RN
RN
RP TISSUE-Bone marrow stroma:
RC MEDLINE=96188248; PubMed=9520411; Yamaguchi K., Kitasaki M., Tsuda E., Yasuda H., Shimizu N., Nakagawa N., Yano K., Goto M., Morizumi S., Tomoyasu A., Yano K., Goto M., Morizumi S., Tomoyasu A., Udagawa N., Takahashi N., Suda T.; Moriyama T., Hashimoto K., Udagawa N., Takahashi N., Suda T.; "Osteocalcin, a bone matrix protein, is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL." Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RL [15] SEQUENCE FROM N.A. (ISOFORM 1).
RN
RN
RP STRAIN=129;
RC MEDLINE=99214075; PubMed=10196481; Strain U., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., Lam U., Wong B.R., Josien R., Choi Y., Blobel C.P.; "Evidence for a role of a tumor necrosis factor- α signaling pathway in the regulation of osteoclastogenesis and dendritic cell survival." J. Biol. Chem. 274:13613-13618(1999).
RL [16] SEQUENCE FROM N.A. (ISOFORMS 1: 2 AND 3).
RN
RN
RP MEDLINE=21150053; PubMed=11250921; Ikeda T., Kasai M., Utsuyama M., Hirokawa K.; "Determination of three isoforms of the receptor activator of nuclear factor- κ B ligand and their differential expression in bone and thymus." Endocrinology 142:1419-1426(2001).
RL [17] SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RN
RN
RP PubMed=10224132;
RX Lam U., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H., Schindler P., Choi Y., Blobel C.P.; "Crystal structure of the TRANCE/RANKL cytokine reveals determinants of receptor-ligand specificity." J. Clin. Invest. 108:971-979(2001).
RT [18] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RL
RN
RN
RP PubMed=11733492;
RX Ito S., Wakabayashi K., Uchikata O., Hayashi S., Okada F., Hata T.; "Crystal structure of the extracellular domain of mouse RANK ligand at 2.2-A resolution." J. Biol. Chem. 277:6631-6636(2002).
RL
RT
RT
CC - FUNCTION: Cytokine that binds to TNFRSF1B/OPG and to TNFRSF1A/RANK. Osteoclast differentiation factor to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of T cell-dependent immune response. May also play an important role in enhanced bone resorption in humoral hypercalcemia of malignancy.

CC -1- SUBUNIT: Homotrimer.
 CC (isoforms 1 and 2): Cytoplasmic (isoform 3).
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
 CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
 CC TRACHEOCULAR BONE AND LUNG.
 CC -1- PTM: N-glycosylated.
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
 CC OF NEMPHORS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS, WITH
 CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
 CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
 CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
 CC HYPERTROPHIC CHONDROCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC use by non-profit institutions. There are no restrictions on its
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF013170; AAC71061.1; -
 CC DR EMBL: AF019048; AAB68812.1; -
 CC DR EMBL: AF053713; AAC40113.1; -
 CC DR EMBL: AB008426; BAA25425.1; -
 CC DR EMBL: AB022039; BAA36970.1; -
 CC DR EMBL: AB022037; BAA36970.1; JOINED.
 CC DR EMBL: AB022038; BAA36970.1; JOINED.
 CC DR EMBL: AB032773; BAA97257.1; -
 CC DR EMBL: AB036798; BAA97259.1; -
 CC DR PDB: 1J72; 12-SEP-01.
 CC PDB: 1J72; 12-SEP-01.
 CC DR MGD: MGI:1100089; Tnfsl1.
 CC DR InterPro: IPR003636; TNF_abcd.
 CC DR InterPro: IPR000478; TNF_family.
 CC DR Pfam: PF00229; TNF_1.
 CC DR SMART: SM00207; TNF_1.
 CC DR PROSITE: PS00251; TNF_1; FALSE_NEG.
 CC DR PROSITE: PS50049; TNF_2; 1.
 CC KW Cytochrome; Differentiation; Receptor; Glycoprotein; Transmembrane;
 CC Signal-anchor, 3D-structure; Alternative splicing.
 CC CHAIN 1 316
 CC
 CC DOMAIN 139 316
 CC TRANSMEM 49 69
 CC
 CC DOMAIN 70 316
 CC SITE 138 316
 CC CARBOHYD 197 197
 CC VARSPLIC 262 262
 CC VARSPLIC 1 117
 CC VARSPLIC 14 44
 CC
 CC CONFLICT 99 99
 CC CONFLICT 141 143
 CC SEQUENCE 316 AA: 34944 MW: 08D65A2BE00967A CMC64;
 CC
 CC Query Match
 CC Best Local Similarity 38.7% Score 176; DB 1; Length 316;
 CC 55.4% Pred. No. 4.4e-13;

Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
 Qy 17 SISFAHRTSSSKRHODANVSNMTFSNGKLRK--GIYNNADICSRHRTVSAGLTL 74
 Db 173 SIPGSKHVLISWYSHDRGMAKISNMTLSNGKLRVNDGFFVYLVNICHFHETSISGPT 232
 Qy 75 QDQL 79
 Db 233 DYQL 237
 RESULT 4
 CSD2_DROME
 ID CSD2_DROME STANDARD; PRT; 501 AA.
 AC Q9VMT6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Probable cytochrome P450 28d2 (EC 1.14.--) (CYP28D2)
 GN CYP28D2 OR CG6081.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga C., Anisimova S., Binkley S., Brodeur G.M., Burtis K.C.,
 RA George R.A., Lewis S.E., Li P.W., Hinkins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H., Blake R.G., Chapple M., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fodor C., Evangelista C.C., Ferraz N.S., Gerhart J., Gerhart J.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Plittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shne B.C., Sidman Klamas I., Simpson M., Skupski M.P., Smith T.,
 RA Spradling A.C., Stappleton M., Strong R., Sun E., Wang Z.-Y.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RA Nelson B.;
 RP Unpublished observations (SEP-2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND
 CC IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).

the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DB DR EMBL; Z22570; CAA80293.1; -;
DR InterPro: IPR002778; SRP19.
DR Pfam; PF01922; SRP19; 1.
DR Prodom; PD006609; SRP19; 1.
KW Signal recognition Particle; RNA-binding; Ribonucleoprotein.
SEQUENCE 310 AA; 35487 MW; D5EC9FC08011AC3 CRC64;

SQ Query Match Score 66; DB 1; Length 310;
Best Local Similarity 41.5%; Pred. No. 2.4; Indels 14; Gaps 3;
Matches 17; Conservative ?; Mismatches 52

OY 12 LLIPSTSHAEKTSLSMKHDDMANVSNMFPNSGKLRYK 52
Db :| || | ||||| | ||||| :| ||:
161 MLTLPSTI-YEAHKR-HPKDMAN-PGRVRFO 187

RESULT 6
NDSM_ALLMA STANDARD; PRT; 641 AA.

ID NDSM_ALLMA
DT P50365; Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DI 01-OCT-1996 (Rel. 34, last annotation update)
DT 15-DEC-1998 (Rel. 37,
DE NAHD-ubiquitinone oxidoreductase chain 5 (Ec 1.6.5.3).
ND5 OR NA.DS.
CN Allomyces macrogynus.
OG Mitochondrion.
OC Eukaryota; Fungi; Chytridiomycota; Blastocladiaceae; Blastocladiales;
NCBI_TaxID=28583; Allomyces.
RX NCBI_TaxID=28583; [1]
RA SEQUENCE FROM N.A.
RP STRAIN-ATCC 46923 / BURMA 3-35 (350C);
RC Paquin B., Roeber I., Wang Z., Lang B.F.;
RL "A robust fungal phylogeny using the mitochondrially encoded nad5
protein sequence";
RT Can. J. Bot. 73:S180-S185(1995).
RN [2]

RX MEDLINE=96226032; Pubmed=8638971;
RA Paquin B., Lang B.F.;
RP "The mitochondrial DNA of Allomyces macrogynus: the complete genomic
sequence from an ancestral fungus".
RT J. Mol. Biol. 255:688-701(1996).

RI -J. CAVALITIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on how
it can be used by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.isb-sib.ch/annotate/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).

DB CC EMBL; U17010; AAB05846.1; -;
DR EMBL; UA1288; AAC49228.1; -;
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPRO01750; Oxidored_qt_
DR InterPro: IPRO01516; Oxidored_qt_N.
DR Pfam; PR00361; oxireded_qf; 1.
PFam; PF00662; oxireded_qf_N; 1.
DR PRINTS; PR01434; NADPHGNASB5.
RW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
KW OxiReductase; NAD; 70674 MW; 9C6AC37EB7E7E61 CRC64;
SQ SEQUENCE 641 AA; 14.4k; Score 65.5; DB 1; Length 641;

```

Best Local Similarity 27.9%; Pred. No. 6.5;
Matches 19; Conservative 12; Mismatches 28; Indels 9; Gaps 2;

OY 2 AITLSTGLILIPISSEAHK-----ISLSSWKHDODW-ANVSMFNSCKLAVK 52
Db 522 SLGLSLALIVAKDKKKHSHKPEGLNVTNTRMLSSKSYWFDVNTYVLISGLHFG 581
OY 53 GIVYRNAD 60
||:|:|:|
Db 582 GIVARDID 589

RESULT 7
Y108-CHLTR
ID Y108-CHLTR STANDARD; PRT; 251 AA.
AC 084110;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN CT108.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/TW-3/Cx;
RX MEDLINE=95000809; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
CC CC
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL: AE001284; AAC67699.1;
CC DR PHC1-2DPAC: 084110;
CC DR InterPro: IPR002678; DUF34.
CC DR Pfam: PF01784; DUF34; 1.
CC DR TIGRFAMs: TIGR00486; DUF34; 1.
CC KW Complete proteome.
CC SQ SEQUENCE 251 AA; 27474 MW; AAC2F6BE7517298E CRC64;

Query Match 14.3%; Score 65; DB 1; Length 251;
Best Local Similarity 26.4%; Pred. No. 2.5;
Matches 23; Conservative 13; Mismatches 27; Indels 24; Gaps 4;

OY 7 SLGLILIPISSEAHKTSLSWK--HDDKNAVSMFNSCKLAVKGI----- 54
Db 91 NIQLIAVHLPL--DAHTTGNMKKVARDKGWSLSEFSSGSPSLGKGVFPEMEVHDEI 147
OY 55 -----YRNADIC--SKRVTISAGI 72
||:|:|:|
Db 148 SOLSAVYQTPVLLAKALGKRRVSSAL 174

RESULT 8
GUB-CLOTM
ID GUB-CLOTM STANDARD; PRT; 334 AA.
AC P29716; P37074;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)

(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (lichenase) (Laminarinase).
GN LICH OR LAM1.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27405 / DSM 1237;
RX MEDLINE=92155194; PubMed=1740123;
RA Schilling S., Schwarz W.H., Staudenbauer W.L.;
RT "Structure of the Clostridium thermocellum gene lcb and the encoded
RT beta-1,3-1,4-glucanase. A catalytic region homologous to Bacillus
RT lichenases joined to the reiterated domain of clostridial
RT cellulases."
RL Eur. J. Biochem. 204:13-19(1992).
RN [2]
RP PRELIMINARY SEQUENCE FROM N.A.
RC STRAIN-E7;
RX MEDLINE=92095946; PubMed=1755832;
RA Zverlov V.V., Laptev D.A., Tishkov V.I., Velikodvorskaja G.A.;
RT "Nucleotide sequence of the Clostridium thermocellum laminarinase
RT gene."
RL Biochem. Biophys. Res. Commun. 181:507-512(1991).
RN [3]
RP REVISIONS.
RA Zverlov V.V.;
RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RA Zverlov V.V., Velikodvorskaja G.A.;
RT "Cloning the Clostridium thermocellum thermostable laminarinase gene
RT in Escherichia coli; the properties of the enzyme thus produced."
RL Biochemol. Lett. 12:811-816(1990).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
CC in beta-D-glucans containing 1,3- and 1,4-bonds.
CC -1- SUBUNIT: MAY FORM PART OF A MULTIMERIC COMPLEX (CELLULOSE).
CC WELL AS IN OTHER C.THERMOCCELLUM CELLULOSE ENZYMES. THIS DOMAIN
CC MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.
CC -1- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL: X63355; CAA44959.1;
CC DR EMBL: X58392; CAA41281.1;
CC DR PIR: S23498; S23498.
CC DR PIR: S20611; JS0611.
CC DR HSSP: P23904; S18726.
CC DR InterPro: IPR002105; Dockerin_1.
CC DR InterPro: IPR002048; EF-hand.
CC DR Pfam: PF00722; Glyco_hydro_16.
CC DR Pfam: PF00722; Glyco_hydro_16; 1.
CC DR PRINTS: PR00737; GLHYDRLASE16.
CC DR PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
CC DR PROSITE: PS00018; EF_HAND_UNKNOWN_2.
CC DR PROSITE: PS00448; CLOS_CELLULOSE_RPT_2.
CC KW Hydrolyase; Glycosidase; Signal; Repeat.
CC FT SIGNAL 1 27
CC FT CHAIN 28 334
CC FT ACT_SITE 136 136
CC FT ACT_SITE 140 140
CC FT DOMAIN 252 269
CC FT DOMAIN 273 331
CC 2 X 24 AA APPROXIMATE REPEATS.

```



```

QY      33 DQDMANVSNNMFTSNGKLRVKGIIYRN--ADICSRHVRTSAGL 72
      1 : : : : | | | | | : | | | :
DB      90 DRKFADIGNIV---KLOYKGGIYRTSKWADITNAHGVTGAGI 128

```

GN ILB.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
CC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Metatheria; Diprodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99221044; PubMed-10206203;
RA Medlock D.N., Goh L.P., Parlane N.A., Buddle B.M.;
RT "Molecular cloning and physiological effects of brushtail possum
interleukin-beta";
RL Vet. Immunol. Immunopathol. 67:359-372(1999).
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: MONOMER.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF071539; AAD21871.1; -
DR HSSP: P01584; 1HTB.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR003502; IL1_propep.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF00394; IL1_propep; 1.
DR PRINTS: PR00262; ILHBGF.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
DR CYCline: Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112 BY SIMILARITY.
FT CHAIN 1 112 INTERLEUKIN-1 BETA.
SQ SEQUENCE 269 AA; 3141 MW; 307A1FE3B627D67 CRC64;

Query Match 13.5%; Score 61.5; DB 1; Length 269;
Best Local Similarity 27.3%; Pred. No. 6.9;
Matches 24; Conservative 13; Mismatches 34; Indels 17; Gaps 4;

QY 12 LLLPSISHEAHKTSLS--KKHDDNVANVSNGKLRVKGYYRNADI---CSRHR 66
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 VMVVALEKMKHNGLSGFOFNDLMNIFNIFQF-----EPITFKNDIYESDSFRL 122
QY 67 VTSAGLTLDLQWLC-----NLRITH 87
DB : : : : : : : : : : : : : : : : : : : : : :
DB 123 VSSQDCTIQDINOKCLASRASELRALH 150

RESULT 12
IPNS STRCL STANDARD; PRT; 329 AA.
AC P10621:
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Isopenicillin N synthetase (EC 1.-.-.-) (IPNS) (Isopenicillin N
DE synthase).
GN PCBC.
OS Streptomyces clavuligerus.
OC Bacteria: Actinobacteria: Actinobacteria (class): Actinobacteridae:
OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
OX NCBI_TaxID=1901;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
RX MEDLINE-98212175; PubMed-1130293;
RA Leski B.K., Aharonowitz Y., Meyerech M., Wolfe S., Vining L.C.,
RA Westlake D.W.S., Jensen S.E.;
RT "Cloning and nucleotide sequence determination of the isopenicillin N
RT synthetase gene from Streptomyces clavuligerus.";
RL Gene 62:187-196(1988).
CC -I- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS
CC FROM DELTA-L-(ALPHA-AMINODIPYL)-L-CYSTEINYL-D-VALINE (ACV) TO
CC FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
CC -I- COFACTOR: IRON AND ASCORBATE.
CC -I- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND
CC CEPHALOSPORIN.
CC -I- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC OXIDOREDUCTASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M19421; AAA26770.1; -
DR EMBL: A01132; CAA00131.1; -
DR PIR: A29894; A29894.
DR HSSP: P05326; 1BLZ.
DR InterPro: IPR005123; 2OG-Ferri_Oxy.
DR InterPro: IPR002283; IPNS_synth.
DR InterPro: IPR002057; Isopen_N_synth.
DR Pfam: PF03171; 2OG-Ferri_Oxy; 1.
DR PRINTS: PR00682; IPNSYNTHASE.
DR PROSITE: PS00185; IPNS_1; 1.
DR PROSITE: PS00186; IPNS_2; 1.
DR Antibioc biosynthesis; Oxidoreductase; Iron; Vitamin C.
FT METAL 212 212 IRON (BY SIMILARITY).
FT METAL 214 214 IRON (BY SIMILARITY).
FT METAL 268 268 IRON (BY SIMILARITY).
SQ SEQUENCE 329 AA; 36958 MW; 71AA1CE9514761C CRC64;

Query Match 13.5%; Score 61.5; DB 1; Length 329;
Best Local Similarity 24.0%; Pred. No. 8.7;
Matches 18; Conservative 12; Mismatches 36; Indels 9; Gaps 2;

QY 15 IPSISHEAHKTSLSWKHD-----QDWNANVSNGKLRVKGYYRNADICSRH 65
DB : : : : : : : : : : : : : : : : : : : : : :
DB 55 LQDVNVEFGAMTDQEKHDLAIHAVPNPVRNGYKAVPORKAVESFCYILNPDGSDH 114
QY 66 RYTSAGLTLDLQW 80
DB : : : : : : : : : : : : : : : : : : : : : :
DB 115 PMTAASTPMHEVNLW 129

RESULT 13
CYAT BOVIN STANDARD; PRT; 1078 AA.
AC Q29450: 002856;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylyl cyclase, type VII (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Adenylyl cyclase).
GN ADCT7.
OS Bos taurus (Bovine).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae.
OC Bovidae: Bovinae: Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

```



```

RC TISSUE=Retina;
RA MEDLINE=96149441; PubMed=8557110;
RT Voelkel H., Beltz E., Klump S., Schultze J.E.;
RT "Cloning and expression of a bovine adenyllyl cyclase type VII
RT specific to the retinal pigment epithelium.";
RL FEBS Lett. 378:245-249(1996).
CC -1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL
CC CYCLASE.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE RETINAL PIGMENT
CC EPITHELIUM.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: 249806; CAA89894.1; ALT_INIT.
DR HSP: P26769; IAB8.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 2.
DR SMART: SM00044; CYC; 2.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 2.
KW Lysase; GMP synthetase; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 33 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 34 54 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 95 120 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 197 594 POTENTIAL.
FT TRANSMEM 595 615 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 620 640 POTENTIAL.
FT TRANSMEM 669 688 POTENTIAL.
FT TRANSMEM 718 737 POTENTIAL.
FT TRANSMEM 746 773 POTENTIAL.
FT TRANSMEM 792 812 POTENTIAL.
FT DOMAIN 813 1078 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 781 781 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1078 AA; 120819 MW; 50E89BF08E37FCBB CRC64;

Query Match 13.5%; Score 61.5; DB 1; Length 1078;
Best Local Similarity 20.9%; Pred. No. 34;
Matches 19; Conservative 19; Mismatches 34; Indels 19; Gaps 2;

OY 4 LITSLDIIILISISIEHAKTSLSSWKHDQDANVSNMFTSGKLRVGIYRNADICS 63
DB 739 MSLEKAVLFLVALVAVLVENYPSMOWDCGSHSLGILGTGLT-----SSSSCS 790
OY 64 RHRVTSAGLTL-----ODLQWNTL 83
DB 791 WHLKTMTNFFLVLYFTTLTMSLQDIYTCRL 821

RESULT 14
NUDI_YEAST STANDARD; PRT; 851 AA.
AC P32336; Q08895;
DT 01-OCT-1993 (Rel. 27 Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE NUDI protein.

```

```

GN NUDI OR YOR373W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A.
RA Dulic V., Zanolari B., Riezman H.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Delius H., Hebling U., Hofmann B.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
CC -1- FUNCTION: REQUIRED FOR NUCLEAR DIVISION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X62147; CAA44073.1; -
DR EMBL: 275281; CAA9704.1; -
DR PIR: S19056; S19056.
DR SGD: S0005900; NUDI.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 4.
DR PRINTS: PR00019; LEURCHNPT.
KW Cell cycle.
FT DOMAIN 223 239 POLY-ASN.
FT DOMAIN 266 274 POLY-SER.
FT CONFLICT 5 6 TQ -> SE (IN REF. 2).
SQ SEQUENCE 851 AA; 94103 MW; CB9F0408633C1315 CRC64;

Query Match 13.4%; Score 61; DB 1; Length 851;
Best Local Similarity 23.5%; Pred. No. 30;
Matches 23; Conservative 14; Mismatches 25; Indels 36; Gaps 4;

OY 9 QLTLLIPSSIEHAKTSLSSWKHDQDANVSNMFTSGKLR----- 50
DB 457 QLISILTSKLS-----GPSYDSDWEKILKVDLSRKLNMGMQRLPNVLNLNS 508
OY 51 -----VKGIYRNADI-CSRHRVTSAGLTL--ODLQ 78
DB 509 DNEMNTLEGIPSNVVOLEFCSNKNKITSAGHSLAGFDLE 546

RESULT 15
GLTI_YEAST STANDARD; PRT; 2144 AA.
AC Q12680; Q12290;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE Glutamate synthase [NADPH] precursor (EC 1.4.1.13) (NADPH-GOGAT).
GN GLTI OR YDL171C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA STRAIN=CN36;
RC STRAIN=CN36;
RX MEDLINE=97082505; PubMed=8923741;
RA Filetici P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P.;
RT "Sequence of the GLTI gene from Saccharomyces cerevisiae reveals the
RT domain structure of yeast glutamate synthase.";
RL Yeast 12:135-136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;

```

RA Pohl T.M.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-oxoglutarate + NADPH.
CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X89221; CAA61505.1; -;
CC DR EMBL: Z67750; CAA91574.1; -;
CC DR EMBL: Z74219; CAA98745.1; -;
CC DR SGD: S0002330; GLT1.
CC DR InterPro: IPR002489; DUF14.
CC DR InterPro: IPR001327; FAD_pyr_redox.
CC DR InterPro: IPR002932; Glu_synthase.
CC DR Pfam: PF00070; Pyr_redox; 1.
CC DR Pfam: PF01493; DUF14; 1.
CC DR Pfam: PF01643; Glu_synthase; 1.
CC DR ProDom: PD000139; FAD_pyr_redox; 1.
CC DR TIGRFAMs: TIGR01317; GOGAT_sm_gam; 1.
CC DR Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
CC KW Glutamate biosynthesis; zymogen.
CC FT PROPEP 1 53
CC FT CHAIN 54 2144
CC FT NP_BIND 1131 1183
CC FT METAL 1184 1184
CC FT METAL 1190 1190
CC FT METAL 1195 1195
CC FT CONFLICT 30 30
CC FT CONFLICT 166 172
CC FT CONFLICT 449 451
CC FT CONFLICT 1752 1752
CC SQ SEQUENCE 2144 AA; 238200 MW; 5AA6A948EF95349 CRC64;
Query Match 13.4%; Score 61; DB 1; Length 2144;
Best Local Similarity 25.6%; Pred. No. 86;
Matches 20; Conservative 19; Mismatches 19; Indels 20; Gaps 6;
QY 5 TLST-QLILLIPSISHEAKTSLSWKHD-----QDANYSNMTFSNGK-----LRVK 52
DB 348 TLSTPEAVMMVPEAYHKDMDSLKAW-YDMAACIMEPWDGPALETFDGRYGAIDLDRN 406
QY 53 GI-----YRNAD---ICS 63
DB 407 GLRPCRYYTSDDRVICA 424

Search completed: December 8, 2002, 19:31:26
Job time : 24.2774 secs

Tue Dec 10 10:51:41 2002

us-09-880-457-4.rpx

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 19:27:28 ; Search time 29.1871 seconds
(without alignments)
286.555 Million cell updates/sec

Title: US-09-880-457-4
Sequence: 1 MALTSLQLILLPSISH.....TSAGLTLQDQLQMCNLRH 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR:***
2: PIR2:***
3: PIR3:***
4: PIR4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	67	14.7	296 2	E72203 conserved hypotet
2	67	14.7	307 2	T46103 conserved hypotet
3	66	14.5	286 2	B96615 probable carbonic
4	65.5	14.4	310 2	JC6516 signal recognition
5	65.5	14.3	641 2	S63645 NMDH2 dehydrogenas
6	65	14.3	210 2	T04933 hypothetical prote
7	65	14.3	251 2	C71557 probable ACR - Chl
8	64.5	14.2	276 2	E36990 probable glucanotr
9	64.5	14.2	427 2	F83984 acetylornithine de
10	64	14.1	334 1	S23498 lichenase (EC 3.
11	63.5	14.0	263 1	S31323 orotidine-5'-phosp
12	63.5	14.0	561 2	AG2336 potassium-dependen
13	63.5	14.0	813 2	F83476 probable sideropho
14	63	13.8	119 2	C64174 hypothetical prote
15	63	13.8	345 2	D97407 conserved hypotet
16	63	13.6	345 2	AE2825 conserved hypotet
17	62	13.6	329 2	T47869 isopenicillin N sy
18	61.5	13.5	329 2	A29894 adenyate cyclase
19	61.5	13.5	1097 2	S68685 glutamate synthase
20	61.5	13.5	2145 2	S61041 membrane-bound lyl
21	61	13.4	455 2	AB0534 NMD1 protein - yea
22	61	13.4	851 2	S67285 maltodextrin utili
23	61	13.4	1101 2	AB1340 outer membrane lip
24	60.5	13.3	277 2	H66664 SP6 protein - yea
25	60.5	13.3	286 2	A36468 hypothetical prote
26	60	13.2	274 2	AC1866 glycosyl hydrolase
27	60	13.2	283 2	A12836 probable lipoprote
28	60	13.2	301 2	S73347
29	60	13.2	301 2	S73347

30	60	13.2	354 2	C97614 hypothetical 32.0K
31	60	13.2	785 2	S73098 aminopeptidase (EC
32	59.5	13.1	169 2	D84027 molybdopterin-guan
33	59.5	13.1	216 2	S56421 Probable hexulose-
34	59.5	13.1	216 2	D91275 Probable hexulose-
35	59.5	13.1	216 2	D86116 Probable hexulose-
36	59.5	13.1	561 2	T46845 maltodextrin utili
37	59.5	13.1	2391 2	T15023 K+-transporting AT
38	59.5	13.0	187 2	A27409 carboxymyl-phosphat
39	59	13.0	220 1	T22254 CDP diacylglycerol
40	59	13.0	649 2	T22254 hypothetical prote
41	59	13.0	769 2	T29796 hypothetical prote
42	58.5	12.9	31 2	AC1998 hypothetical prote
43	58.5	12.9	398 2	AC1998
44	58.5	12.9	958 1	JN0102
45	58.5	12.9	958 1	JN0102

ALIGNMENTS

RESULT 1
E72203 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72203
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72203
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <ARN>
A:Cross-references: GB:AE001822; GB:AE000512; NID:94982429; PIDN:AD36914.1; PID:9498
A:Experimental source: strain MSB8
A:Gene: TM1852
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH107

Query Match 14.7% Score 67; DB 2; Length 296;
Best Local Similarity 27.3% Pred. No 5.4;
Matches 15; Conservative 11; Mismatches 19; Indels 10; Gaps 3;

QY 33 DQDW---ANVSNMFSNGKLRVKG---IYRNADICSHRYTSAGTLQDQLQMC 81
DB 244 EDWKEFGGVNPFVSDAMIEYGYVYGAADMC---TALTITPEYKMKMC 294

RESULT 2

T46103 hypothetical protein T25B15.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46103
R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Maché, R.; Mewes, H.W.; Lemke, K.; Mayer,
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23021
A:Accession: T46103
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <ALC>
A:Cross-references: EMBL:AL132972
A:Experimental source: cultivar Columbia; BAC clone T25B15

C:Genetics:
A:Map position: 3
A:Introns: 63/3; 225/2; 267/3
A:Note: T25B15.100
Query Match 14.7% Score 67; DB 2; Length 307;

Best Local Similarity 18.3%; Pred. No. 5.7;
Matches 15; Conservative 19; Mismatches 26; Indels 22; Gaps 2;

OY 20 HEAKTSLSSMKHDOW-----ANYSNMTEFSNGKRVAGIYYRN 58
Db 149 HDEYVLSTYVHNNEMKVRSEHVLVGLARTSMKTKQCHHLPYSQG-TTNGVLYYC 207
OY 59 ADICSRHRYTSAGTLTLOLQ 80
Db 208 AMTDCKVLMSEFDLTSEDVGV 229

RESULT 3

B96615

Probable carbonic anhydrase T18124.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nansen, N.F.; Hughes, B.; Hultner, L.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marshall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzedo, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <570>
A:Cross-references: GB:AE005173; NID:g11038509; PIDN:AAQ27786.1; GSPDB:GN00141
C:Genetics:
A:Gene: T18124.9
A:Map position: 1

Query Match 14.5%; Score 66; DB 2; Length 286;
Best Local Similarity 21.1%; Pred. No. 6.8;
Matches 27; Conservative 22; Mismatches 29; Indels 50; Gaps 7;

OY 2 AITLSLOLILIPIS-----ISHNAKTSLSW-----KHDOD 35
Db 159 AVTTLOVENITVGHSGGIALMSHQHGOHSHRWNGSKAAKLRTOLASSLSFDEQ 218
OY 36 MAN-----VSNN-TFS-----NGKRVAGIYYRNADICSRH-----VTSAGL 72
Db 219 CRNCKESIKDSVNLITYSWIRKVRKGEVKGICYYNLSD-CSEKRWLSDKTYGCF 277
OY 73 TLDDQLM 80
Db 278 YISDREIV 285

RESULT 4

JC6516

Signal recognition particle protein Sec65 - yeast (Yarrowia lipolytica)
N:Alternate names: SRP19
C:Species: Yarrowia lipolytica, Candida lipolytica
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 23-Jul-1999
R:Sanchez, M.; Beckerich, J.M.; Gallard, C.; Dominguez, A.
Gene 203, 75-84, 1997
A:Title: Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a component of the
A:Reference number: JC6516; MUID:96085978; PMID:9426009
A:Accession: JC6516
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <SAND>
A:Cross-references: EMBL:Z22570; NID:g473182; PID:g473183

Query Match 14.5%; Score 66; DB 2; Length 310;

Best Local Similarity 41.5%; Pred. No. 7.5;
Matches 17; Conservative 7; Mismatches 3; Indels 14; Gaps 3;

OY 12 LLLIPISHEAKTSLSSMKHDOWANYSNMTEFSNGKRLRV 52
Db 161 MLTLPST-YEAKT-----HPKDMAN-----FGHVRVQ 187

RESULT 5

S63645

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Allomyces macrogynus mitochon
C:Species: mitochondrion Allomyces macrogynus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
R:Paquin, B.; Lang, B.F.
J. Mol. Biol. 255, 688-701, 1996
A:Title: The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence
A:Reference number: S63645; MUID:96226032; PMID:8636971
A:Accession: S63645
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-641 <PAQ>
A:Cross-references: EMBL:U41288; NID:g1236403; PIDN:AAQ49228.1; PID:g1236411
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Genome: mitochondrion
A:Introns: 144/3; 241/3; 314/1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 14.4%; Score 65.5; DB 2; Length 641;
Best Local Similarity 27.9%; Pred. No. 20;
Matches 19; Conservative 12; Mismatches 28; Indels 9; Gaps 2;

OY 2 AITLSLOLILIPISHEAK-----TSLSKRWHDOW--ANYSNMTEFSNGKRLRV 52
Db 522 SLGSLALVLDPKRMHSIEKPEGLNTVITWMLSKSRFPDNYVTVLLSGSLHFG 581
OY 53 GITYRNAD 60
Db 582 GIFARDID 589

RESULT 6

T04933

Hypothetical protein T9A21.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, February 1999
A:Accession: T04933
A:Molecule type: DNA
A:Residues: 1-210 <BEV>
A:Cross-references: EMBL:AL021713
A:Experimental source: cultivar Columbia; BAC clone T9A21
A:Map position: 4
A:Note: T9A21.160

Query Match 14.3%; Score 65; DB 2; Length 210;
Best Local Similarity 36.0%; Pred. No. 6.2;
Matches 18; Conservative 8; Mismatches 16; Indels 8; Gaps 2;

OY 3 IITLSLOLILIPISHEAKTSLSSMKH-----DQWANSNMTEFS 45
Db 101 IPTNMLPVYGVSTIDISPSADKISITIGWHSFDTFOSQDW-NVTNINVT 149

RESULT 7

C71557

Probable ACR - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Keywords: carbon-carbon lyase; carboxy-lyase
F:3-263/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>

Query Match 14.0%; Score 63.5; DB 1; Length 263;
Best Local Similarity 39.5%; Pred. No. 12;
Matches 17; Conservative 7; Mismatches 12; Indels 7; Gaps 2;

OY 33 DDMANVSNMTFSGKLRVKGIRYRN---ADICSRHRVTSAGL 72
DB 90 DRKFADIGNTV---KLOYKGIYRTSKRADITMAHGVYAGGI 128

RESULT 12

AG2336 potassium-dependent ATPase chain A [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jan-2002
C:Accession: AG2336

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriguen, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:11595285; PMID:11759840
A:Accession: AG2336
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1561 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA075945.1; PID:g1713381; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4246
C:Superfamily: H+/K+-transporting ATPase chain A

Query Match 14.0%; Score 63.5; DB 2; Length 561;
Best Local Similarity 30.1%; Pred. No. 29;
Matches 25; Conservative 11; Mismatches 32; Indels 15; Gaps 3;

OY 1 MAILTSLQILIPISHEAKTSLSSWKHODMANVSNMTFSGKLRVKGIRYRNAD 60
DB 415 LAILLIPYIVLIPISALALAPFSL-----GISNPSFHC-----ISQVVEYAS 461

OY 61 ICSRHVTSAGLTLDDLDLQCNL 83
DB 462 ASANNGSGLEGLT--DNSLMMNL 482

RESULT 13

F83476 Probable siderophore receptor PA1365 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83476

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83476
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-813 <STO>

A:Cross-references: GB:AE004565; GB:AE004091; NID:g9947294; PIDN:AA00454.1; GSPDB:GN00179
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1365

Query Match 14.0%; Score 63.5; DB 2; Length 813;
Best Local Similarity 28.8%; Pred. No. 44;
Matches 19; Conservative 11; Mismatches 23; Indels 13; Gaps 3;

OY 25 TSLSWKHDDMANVSNMTFSGKLRVKGIRYRNADICSRHRVT---SAG 71

DB 711 TAYLOKRPDADMMNRLOATFFDSKDYRLDGVESGRRVSTYTVLVSQYRITPPDQLS 770
OY 72 LITLQDL 77
DB 771 LGIONL 776

RESULT 14

CG4174 hypothetical protein H1656 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C:Accession: CG4174

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehlavag, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gneim, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: CG4174
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-119 <TIGR>
A:Cross-references: GB:032838; GB:L42023; NID:g1574497; PIDN:AA023300.1; PID:g1574505
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: hypothetical protein H1656

Query Match 13.8%; Score 63; DB 2; Length 119;
Best Local Similarity 21.9%; Pred. No. 5.5;
Matches 16; Conservative 19; Mismatches 28; Indels 10; Gaps 3;

OY 10 LILIPISHEAKTSLSS--WKHODMANVSNMTFSGKLRVKGIRYRNADICSRHRV 67
DB 49 IVEVEYRQSHSAVGSALIESVDNRKQKWDANMLAKONMSLE-----DANCRFDL 101

OY 68 TSAGLTLDLQDL 80
DB 102 IAFGKTPDIO-W 113

RESULT 15

D97407 hypothetical protein AGR_C-701 [imported] - Agrobacterium tumefaciens (strain C58, Ce)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: D97407

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, A. Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: D97407
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-345 <KUR>

A:Cross-references: GB:AB007869; PIDN:AA06213.1; PID:g15155314; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C-701
A:Map position: circular chromosome

Query Match 13.8%; Score 63; DB 2; Length 345;
Best Local Similarity 28.0%; Pred. No. 19;
Matches 21; Conservative 14; Mismatches 20; Indels 20; Gaps 5;

OY 12 LILIPISHEAKTSLSSWKHODMANVSNMTFSGKLRVKGIRYRNADICSRHRV 62
DB 144 LTMVPSFVHEL-DVSIPT---PEMGRTV-MDISYG-----GTFYALVDVQIGLTTEKA 192

OY 63 SRHRVTSAGLTLDDL 77
DB 193 NAKLVAAAGMTLKD 207

Tue Dec 10 10:51:41 2002

us-09-880-457-4.rpt

Page 5

Search completed: December 8, 2002, 19:34:43
Job time : 37.1871 secs

2
1
2

Tue Dec 10 10:51:40 2002

us-09-880-457-4.ra1

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2002, 19:30:43 : Search time 18.5226 Seconds
(without alignments)
138.199 Million cell updates/sec

Title: US-09-880-457-4

Perfect score: 455
Sequence: 1 MAILTSLQILLILIPISIH.....TSAGULTLODLMCMRLIHH 87

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, AA:
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6ackfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.5	39.7	317	3	US-08-996-139-13 Sequence 13, Appl
2	180.5	39.7	317	4	US-08-995-659-13 Sequence 13, Appl
3	180.5	39.7	317	4	US-09-215-649A-13 Sequence 4, Appl
4	180.5	39.7	317	4	US-09-052-521C-4 Sequence 13, Appl
5	180.5	39.7	317	4	US-09-577-780-13 Sequence 11, Appl
6	176	38.7	294	3	US-08-995-659-11 Sequence 11, Appl
7	176	38.7	294	4	US-09-215-649A-11 Sequence 11, Appl
8	176	38.7	294	4	US-09-577-780-11 Sequence 7, Appl
9	176	38.7	316	2	US-08-842-842-7 Sequence 2, Appl
10	176	38.7	316	4	US-08-989-362-2 Sequence 2, Appl
11	176	38.7	316	4	US-09-052-521C-2 Sequence 34, Appl
12	176	38.7	28	4	US-09-052-521C-34 Patent No. 5206163
13	168	14.9	1286	6	Sequence 6, Appl
14	68	14.8	490	4	US-09-336-643A-6 Sequence 9, Appl
15	67.5	14.1	279	3	US-09-286-690-9 Sequence 33, Appl
16	64	13.8	376	4	US-09-052-521C-33 Sequence 100, App
17	63	13.8	376	1	US-08-594-031-100 Sequence 102, App
18	63	13.8	376	1	US-08-594-031-102 Sequence 5, Appl
19	63	13.5	329	4	US-08-413-231-5 Sequence 9, Appl
20	61.5	13.5	329	4	US-08-618-911-6 Sequence 6, Appl
21	60.5	13.3	158	2	US-08-184-748-2 Sequence 2, Appl
22	60.5	13.3	721	4	US-08-446-855A-2 Sequence 2, Appl
23	59.5	13.1	2391	2	US-09-150-741-2 Sequence 4, Appl
24	59.5	13.1	2391	2	US-08-763-121-4 Sequence 4, Appl
25	59	13.0	220	4	US-09-216-066-4 Sequence 4, Appl
26	59	13.0			
27	59	13.0			

28	57.5	12.6	525	1	US-08-677-939-17 Sequence 17, Appl
29	57.5	12.6	525	1	US-08-461-599-17 Sequence 17, Appl
30	57.5	12.6	525	1	US-08-461-621-17 Sequence 17, Appl
31	57.5	12.6	525	1	US-08-465-334-17 Sequence 4, Appl
32	56.5	12.4	158	2	US-08-618-911-4 Sequence 2, Appl
33	56.5	12.4	158	3	US-08-938-675A-2 Sequence 10, Appl
34	56.5	12.4	333	4	US-09-413-231-10 Sequence 4, Appl
35	56	12.3	391	4	US-09-200-090-4 Sequence 1, Appl
36	56	12.3	521	2	US-08-933-227-1 Sequence 2, Appl
37	56	12.3	878	4	US-09-735-934A-2 Sequence 93, Appl
38	55.5	12.2	81	2	US-08-332-562A-93 Sequence 1, Appl
39	55.5	12.2	146	4	US-08-637-323-1 Sequence 16, Appl
40	55.5	12.2	149	3	US-08-584-031-16 Sequence 3, Appl
41	55.5	12.2	151	1	US-07-940-605A-3 Sequence 3, Appl
42	55.5	12.2	151	2	US-08-690-096-3 Sequence 2, Appl
43	55.5	12.2	261	1	US-07-940-605A-2 Sequence 8, Appl
44	55.5	12.2	261	1	US-08-184-422-8 Sequence 2, Appl
45	55.5	12.2	261	1	US-08-360-923A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-13
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

Query Match 39.7%; Score 180.5; DB 3; Length 317;
Best Local Similarity 59.7%; Pred. No. 3.4e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

OY 15 IPSISHEAKTSLSSKRDODMANVSNMTFSGKLRV--GIYRNADICSRHRTSAGL 72
DB 175 IPSGS---HKVSLSSWYHDRGMAKISNMTFSGKLIYNODGFTYLYANICFRHHTSGDL 231

OY 73 TIQDLQL 79
DB 232 ATEYLQL 238

RESULT 2
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-13

Query Match 39.7%; Score 180.5; DB 4; Length 317;
Best Local Similarity 59.7%; Pred. No. 3.4e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

OY 15 IPSISHEAKTSLSSKRDODMANVSNMTFSGKLRV--GIYRNADICSRHRTSAGL 72
DB 175 IPSGS---HKVSLSSWYHDRGMAKISNMTFSGKLIYNODGFTYLYANICFRHHTSGDL 231

OY 73 TIQDLQL 79
DB 232 ATEYLQL 238

RESULT 3
US-09-215-649A-13
; Sequence 13, Application US/09215649A
; Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

Query Match 39.7%; Score 180.5; DB 4; Length 317;
Best Local Similarity 59.7%; Pred. No. 3.4e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

OY 15 IPSISHEAKTSLSSKRDODMANVSNMTFSGKLRV--GIYRNADICSRHRTSAGL 72
DB 175 IPSGS---HKVSLSSWYHDRGMAKISNMTFSGKLIYNODGFTYLYANICFRHHTSGDL 231

OY 73 TIQDLQL 79
DB 232 ATEYLQL 238

RESULT 4
US-09-052-521C-4
; Sequence 4, Application US/09052521C
; Patent No. 6316408
GENERAL INFORMATION:

LENGTH: 317 amino acids

Query Match	38.7%;	
Best Local Similarity	55.4%;	
Matches	36;	Conservative
		Indels
		Gaps

QY 17 SISHEAKTSLSSWKHDODMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGTL 74
DB 151 SIPSGSHKVTLSWYHDKRMAKISNMTLSNGKLRVNDGFFYLYANICFRHHEHETSGSVPT 210
QY 75 QDIQL 79
DB 211 DYLOL 215

RESULT 7

US-08-995-659-11
Sequence 11, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-11

Query Match
Best Local Similarity 38.7%; Score 176; DB 4; Length 294;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 17 SISHEAKTSLSSWKHDODMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGTL 74
DB 151 SIPSGSHKVTLSWYHDKRMAKISNMTLSNGKLRVNDGFFYLYANICFRHHEHETSGSVPT 210
QY 75 QDIQL 79
DB 211 DYLOL 215

RESULT 8

US-09-215-649A-11
Sequence 11, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match
Best Local Similarity 38.7%; Score 176; DB 4; Length 294;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 17 SISHEAKTSLSSWKHDODMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGTL 74
DB 151 SIPSGSHKVTLSWYHDKRMAKISNMTLSNGKLRVNDGFFYLYANICFRHHEHETSGSVPT 210
QY 75 QDIQL 79
DB 211 DYLOL 215

RESULT 9

US-09-577-780-11
Sequence 11, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

QY 17 SISHEAKTSLSSWKHDODMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTSAGTL 74
DB 151 SIPSGSHKVTLSWYHDKRMAKISNMTLSNGKLRVNDGFFYLYANICFRHHEHETSGSVPT 210
QY 75 QDIQL 79
DB 211 DYLOL 215

Best Local Similarity 55.4%; Pred. No. 1.3e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

OY 17 SISHEAKTSLSSMKHODMANVSNMTPFSGKLRVK--GIYYNADICSRHRTSAGLTL 74
Db 173 SIPSQSHKVTLSWYHNRGMAKISNMTLSNGKLRVNODGFYLYANICFRHHTSGSVPT 232

OY 75 QDIQL 79
Db 233 DYQL 237

RESULT 12

US-09-052-521C-2
Sequence 2, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451BIV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 316
TYPE: PRT
ORGANISM: Mouse
US-09-052-521C-2

Query Match 38.7%; Score 176; DB 4; Length 316;
Best Local Similarity 55.4%; Pred. No. 1.3e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

OY 17 SISHEAKTSLSSMKHODMANVSNMTPFSGKLRVK--GIYYNADICSRHRTSAGLTL 74
Db 173 SIPSQSHKVTLSWYHNRGMAKISNMTLSNGKLRVNODGFYLYANICFRHHTSGSVPT 232

OY 75 QDIQL 79
Db 233 DYQL 237

RESULT 13

US-09-052-521C-34
Sequence 34, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451BIV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-052-521C-34

Query Match 16.7%; Score 76; DB 4; Length 28;

Best Local Similarity 54.2%; Pred. No. 0.0037;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 17 SISHEAKTSLSSMKHODMANVSNMTPFSGKLRVK--GIYYNADICSRHRTSAGLTL 74
Db 4 SIPSQSHKVTLSWYHNRGMAKISNMTLSNGKLRVNODGFYLYANICFRHHTSGSVPT 27

RESULT 14

5206163-1
Patent No. 5206163
APPLICANT: RENARD, ANDRE;DINA, DINO;MARTIAL, JOSEPH
TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA
VIRUS PROTEIN
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/550,816
FILING DATE: 06-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 331,037
FILING DATE: 29-MAR-1989
APPLICATION NUMBER: 752,981
FILING DATE: 08-JUL-1985
SEQ ID NO:1
LENGTH: 1286
5206163-1

Query Match 14.9%; Score 68; DB 6; Length 1286;
Best Local Similarity 23.4%; Pred. No. 6.1e-11;
Matches 25; Conservative 18; Mismatches 22; Indels 42; Gaps 4;

OY 1 MAILTSLQIL-----LILPISH-----EAKTSLSSMKHQ 34
Db 1196 MAVLTLLMLSYTDYRKYRMLOCLISLAGVFLIRSLKHLGEIPELTPWRR--- 1252

OY 35 DWANVSNMTPFSGKLRVKGIYYNADICSRHRTSAGLTLQIOWC 81
Db 1253 -----PLTFL-----LTLTATVTRKWKVDIAGLILQPOSFC 1286

RESULT 15

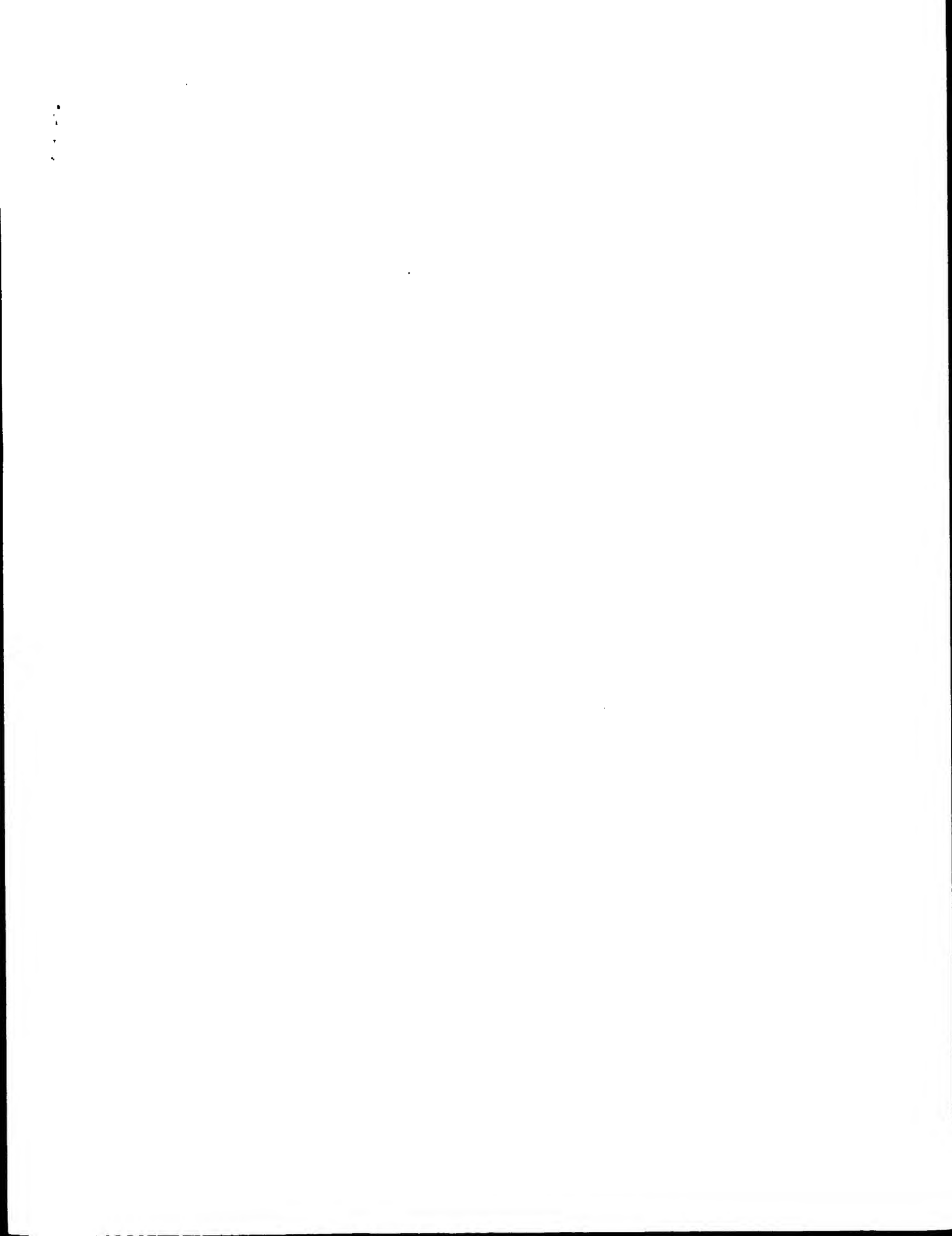
US-09-336-643A-6
Sequence 6, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 490
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643A-6

Query Match 14.8%; Score 67.5; DB 4; Length 490;
Best Local Similarity 22.0%; Pred. No. 2e-05;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

OY 1 MAILTSLQILILPISHAKTSLSS-----WKHODMANVSNMTPFSGKLRVKGIY 55

Db 328 LLELSVGISIFSVLYISVEKDHFTSSLTSLPICW-----WATISMVTYVG----- 374
Qy 56 YRNADICSRHRYTSAGLTLQDLQMCNLRIT 86
Db 375 -----DTHPVTLAGKLIASCTICGILYV 398

Search completed: December 8, 2002, 19:35:31
Job time : 20.5226 secs



OM protein - protein search, using sw model
December 8, 2002, 17:26:33 : Search time 52.7613 Seconds
219,722 Million cell updates/

ne-09-880-457-4

Sequence:

Scoring table

Searched: 908470 seqs, 1352000
bits satisfying chosen parameters

Total number of files: 0

Minimum	DB	seq	length:	2000000000
Minimum	DB	seq	length:	2000000000
Maximum	DB	seq	length:	2000000000
Minimum	Match	0%		
Minimum	Match	0%		
Minimum	Match	0%		

post-processing:	Maximum	Match	100%
	Maximum	first	45 summaries
listing			

Database

```

MAKING FIRST 43 SEQUENCES
Listing first 43 sequences
A. Genseq-101002.*
1: /SID52/gcgdata/genseq/genseqp-emb1/AA1980.DAT.*
2: /SID52/gcgdata/genseq/genseqp-emb1/AA1981.DAT.*
3: /SID52/gcgdata/genseq/genseqp-emb1/AA1983.DAT.*
4: /SID52/gcgdata/genseq/genseqp-emb1/AA1984.DAT.*
5: /SID52/gcgdata/genseq/genseqp-emb1/AA1985.DAT.*
6: /SID52/gcgdata/genseq/genseqp-emb1/AA1987.DAT.*
7: /SID52/gcgdata/genseq/genseqp-emb1/AA1988.DAT.*
8: /SID52/gcgdata/genseq/genseqp-emb1/AA1989.DAT.*
9: /SID52/gcgdata/genseq/genseqp-emb1/AA1990.DAT.*
10: /SID52/gcgdata/genseq/genseqp-emb1/AA1992.DAT.*
11: /SID52/gcgdata/genseq/genseqp-emb1/AA1993.DAT.*
12: /SID52/gcgdata/genseq/genseqp-emb1/AA1995.DAT.*
13: /SID52/gcgdata/genseq/genseqp-emb1/AA1996.DAT.*
14: /SID52/gcgdata/genseq/genseqp-emb1/AA1997.DAT.*
15: /SID52/gcgdata/genseq/genseqp-emb1/AA1999.DAT.*
16: /SID52/gcgdata/genseq/genseqp-emb1/AA1998.DAT.*
17: /SID52/gcgdata/genseq/genseqp-emb1/AA1999.DAT.*
18: /SID52/gcgdata/genseq/genseqp-emb1/AA2000.DAT.*
19: /SID52/gcgdata/genseq/genseqp-emb1/AA2001.DAT.*
20: /SID52/gcgdata/genseq/genseqp-emb1/AA2002.DAT.*
21: /SID52/gcgdata/genseq/genseqp-emb1/AA2001.DAT.*
22: /SID52/gcgdata/genseq/genseqp-emb1/AA2002.DAT.*
23: /SID52/gcgdata/genseq/genseqp-emb1/AA2002.DAT.*

```

pred. No. is the number of the total score greater than or equal to and is derived by analysis of the

SUMMARIES

Description-----

Result	Score	Query Match	length	DB	ID	
NO.						
1	44.0	96.7	95	23	AAU083632	Human PRO proteome
2	181	39.8	170	22	AAU08386	Mouse FLAG-mul
3	180.5	39.7	152	22	AAU08386	Human RANKL
4	180.5	39.7	160	21	AAU08386	Human acid sequenc
5	180.5	39.7	244	23	AAU08386	Human TRANCE polyp
6	180.5	39.7	246	23	AAU08386	Human TRANCE polyp
7	180.5	39.7	246	23	AAU08386	Human TRANCE polyp
8	180.5	39.7	317	19	AAU08386	Human TRANCE polyp
9	180.5	39.7	317	19	AAU08386	Human TRANCE polyp
10	180.5	39.7	317	19	AAU08386	Human TRANCE polyp

11	180.5	39.7	317	19	PAW68293
12	180.5	39.7	317	21	PAE08417
13	180.5	39.7	317	22	PAE08438
14	180.5	39.7	317	22	PAE04456
15	180.5	39.7	317	22	PAE01993
16	180.5	39.7	317	23	PAE08134
17	180.5	39.7	317	23	PAU78285
18	180.5	39.7	318	22	PAU78292
19	177.5	38.7	245	20	PAU17873
20	176.5	38.7	160	21	PAE08272
21	176.5	38.7	173	21	PAE08441
22	176.5	38.7	173	21	PAE08445
23	176.5	38.7	173	21	PAE08442
24	176.5	38.7	182	21	PAE84420
25	176.5	38.7	187	21	PAE84420
26	176.5	38.7	187	21	PAE84423
27	176.5	38.7	188	21	PAE83019
28	176.5	38.7	244	19	PAE68956
29	176.5	38.7	294	19	PAE68292
30	176.5	38.7	294	19	PAE08737
31	176.5	38.7	294	22	PAE04425
32	176.5	38.7	294	22	PAE01992
33	176.5	38.7	294	22	PAE83194
34	176.5	38.7	294	22	PAE83017
35	176.5	38.7	316	19	PAE83117
36	176.5	38.7	316	19	PAE83117
37	176.5	38.7	316	19	PAE83117
38	176.5	38.7	316	19	PAE83117
39	176.5	38.7	316	19	PAE83117
40	176.5	38.7	316	19	PAE83117
41	176.5	38.7	316	19	PAE83117
42	176.5	38.7	316	19	PAE83117
43	176.5	38.7	316	19	PAE83117
44	176.5	38.7	316	19	PAE83117
45	176.5	38.7	316	19	PAE83117

ALIGNMENTS

RESULT I
ID A083632 standard; protein: 95 aa.
XX AC A083632;
XX DT 08-MAY-2002 (first entry)
DE Human PRO protein, Seq ID No 82.
KM breast cancer; prostate tumour; liver tumour;
KM pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor alpha.

Homo sapiens.
OS Homo sapiens.
XX WO200208288-A2.
XX 31-JAN-2002.
PD 29-JUN-2001; 2001WO-US21066.
XX 29-JUN-2001; 2003US-219556P.
PE 20-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220866P.
PR 25-JUL-2000; 2000US-220883P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.

NF-KB receptor act
 Amino acid sequenc
 Human receptor act
 Human receptor act
 Human full-length
 Human RANKL polype
 Human TRANCE prote
 Human TRANCE dif
 Rat osteoclast hom
 Human TRANCE hom
 Amino acid sequenc
 Amino acid sequenc
 DNA encoding osteo
 An osteoprotegerin
 Amino acid sequenc
 An osteoprotegerin
 An osteoprot-blind
 A murine OCIF-blind
 NF-KB receptor act
 NF-KB receptor act
 Murine receptor ac
 Murine receptor ac
 Murine RANKL (rece
 Murine osteoprotege
 Human osteogenesis
 Osteoclasts sequenc
 Amino acid sequenc
 Murine TRANCE. Mu
 Murine OBK protein
 Mouse OBK sequenc
 Amino acid sequenc
 Amino TRANCE prote
 Mouse fibronectin
 GlutathioneS-T-modf fu
 Amino acid sequenc
 Murine OBK protein
 Mouse OBK sequenc
 A murine osteoprot
 An osteoprotegerin

PR 23-AUG-2000; 2000MO-US23532.
 PR 24-AUG-2000; 2000MO-US23532.
 PR 15-SEP-2000; 2000MO-US23532.
 PR 10-NOV-2000; 2000MO-US23532.
 PR 28-NOV-2000; 2000MO-US23532.
 PR 01-DEC-2000; 2000MO-US23532.
 PR 20-DEC-2000; 2000MO-US23532.
 PR 20-DEC-2000; 2000MO-US23532.
 PR 28-FEB-2001; 2001MO-US054280.
 PR 10-MAY-2001; 2001MO-US054280.
 PR 25-MAY-2001; 2001MO-US054280.
 PA (GETH) GENENTECH INC.
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT,
 DR WPI: 2002-172001/22.
 DR N-PSDB: ABK33576.
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumour,
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PS tumour or liver tumour.
 PS Claim 11: Figure 82; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polypeptides
 CC encode human secreted proteins. The PRO polypeptides are useful
 CC for diagnosing tumours, rectal tumour, prostate tumour, breast
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour,
 CC liver tumour, lung cancer, breast tumour, prostate tumour, rectal
 CC tumour, colon cancer, breast tumour, prostate tumour, rectal tumour,
 CC for stimulating the release of tumour necrosis factor- α from human dermal
 CC fibroblast cells or inhibiting the proliferation of tumour cells, for
 CC stimulating the release of tumour necrosis factor- α from human dermal
 CC fibroblast cells or inhibiting the proliferation of tumour cells, for
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. The PRO nucleic acids have
 CC protein sequences of the invention. AU083392-AU083713 represent human PRO
 SO Sequence 95 AA.
 Query Match
 Best Local Similarity 96.7%; Score 440; DB 23; Length 95;
 Matches 84; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 MAILTSLQILLLIPSHRAKTSLSKRDHDMANVSNMTFSNGKLRVKGYYRNAD 60
 DB 1 MAILTSLQILLLIPSHRAKTSLSKRDHDMANVSNMTFSNGKLRVKGYYRNAD 60
 OY 61 ICSRRHTVSGTLTDLQMLCMTARTI 86
 DB 61 ICSRRHTVSGTLTDLQMLCMTARTI 86
 RESULT 2
 ID AU08386 standard; Protein, 170 AA.
 AC AU08386;
 DE 17-DEC-2001 (first entry)
 DE Mouse FLAG-murine Opcbp[158-316].
 KW Antibody; Opcbp; osteoprotegerin; FLAG-murine Opcbp[158-316].
 KW Osteoprotegerin binding protein; osteoclast formation;
 KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
 KW bone cancer; Rheumatoid arthritis; hypercalcaemia of malignancy;

KW Steroid-induced osteoporosis; mutant; mutein.
 OS Mus sp.
 OS Synthetic.
 FH Key
 FT Peptide
 FT Msc-difference
 FT Misc-difference 83..87
 FT /note: "Note wild-type Ser-Val-Pro-Thr-Asp
 PN substituted by Asp-Leu-Ala-Thr-Glu"
 PD W0200162932-A1.
 PS 30-AUG-2001.
 PR 23-FEB-2001; 2001MO-US05973.
 PR 23-FEB-2000; 2000US-0511139.
 PR 22-FEB-2001; 2001US-0791153.
 PA (AMGE-) AMGEN INC.
 PI Deshpande RV, Hitz A, Boyle WJ, Sullivan JK,
 DR WPI: 2001-557706/62.
 DR N-PSDB: AAS13369.
 CC Antibodies that bind antagonistically to osteoprotegerin binding
 CC protein, useful for treating osteoporosis, metastasis of cancer to
 CC bone, rheumatoid arthritis, hypercalcaemia of malignancy and
 CC steroid-induced osteoporosis.
 CC Example 10; Fig 28; 239pp; English.
 CC The invention relates to an antibody or antigen binding domain (or
 CC fragment, variant or derivative) which binds to an osteoprotegerin
 CC binding protein (Opcbp) and which is an osteoprotegerin (or
 CC osteoclast) formation or activation domain may be administered to
 CC prevent or treat loss of bone mass in a mammal and to prevent or treat
 CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
 CC hypercalcaemia of malignancy and to prevent or treat
 CC present sequence encodes FLAG-murine Opcbp[158-316].
 SO Sequence 170 AA;
 Query Match
 Best Local Similarity 39.8%; Score 181; DB 22; Length 170;
 Matches 37; Conservative 6; Mismatches 20; Indels 2; Gaps 1;
 OY 17 SISRAHRTSLSSWKHDQMANVSNMTFSNGKLRV--GIYRNADICSHRYTSAGTL 74
 DB 27 SIPGSHRYTSLSWKHDQMANVSNMTFSNGKLRV--GIYRNADICSHRYTSAGTL 74
 OY 75 ODOL 79
 DB 87 EYOL 91
 RESULT 3
 ID AAB67248 standard; Protein, 152 AA.
 AC AAB67248;
 DE 18-APR-2001 (first entry)
 DE Human RANKL.
 KW Human; Apo2 ligand; divalent metal ions; viral infection; cancer.

OS	Homo sapiens.
XX	
PN	WO200100832-A1.
XX	
PD	04-JAN-2001.
XX	
PF	26-JUN-2000; 2000WO-US17579.
XX	
PR	28-JUN-1999; 99US-0141342.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Hymowitz S, Kelley RE, Koumenis I, Leung S;
XX	O'Connell M, Pal R, Shahrokh Z, Simmons L;
DR	WPI: 2001-123012/13.
XX	
PT	Use of divalent metal ions for making Apo-2 ligand and in formulations
PR	containing Apo-2 ligand for increasing yield and stability of ligand
PT	trimers, useful for therapeutic applications -
XX	
PS	Disclosure: Fig 3; 60pp; English.
XX	
CC	The present invention relates to a formulation comprising Apo-2
CC	ligand and divalent metal ions. Apo-2 ligand and the formulation
CC	are useful for treating cancers and viral infections. Addition
CC	of divalent metal ions for making Apo-2 ligand and formulations
CC	containing Apo-2 ligand results in increased yield and stability
CC	of Apo-2 ligand trimers.
XX	
SQ	Sequence 152 AA:
	Query Match 39.7%; Score 180.5; DB 22; Length 152;
	Best Local Similarity 59.7%; Pred.No. 8,le-15;
	Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2
OY	15 IPSISHEAHKTSLSWKHDQMANVSNMTFSNGCLRVK--GIYYRNADICSRHRTSAGL 72 : : : : Db 13 IPSGS---HKVSLSSWMYHRCGAKISNMTFNSGKLIVNQDGFYLYLVANICFRHHETSGL 69
OY	73 TLDDQL 79 : Db 70 ATEYLQL 76
RESULT 4	
AA080273	
ID	AA080273 standard; Protein: 160 AA.
XX	
AC	AA080273:
XX	
DT	04-DEC-2000 (first entry)
DE	
XX	Amino acid sequence of a human TNF ligand QPGL.
XX	
KW	AGE-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; Type II transmembrane protein; B cell stimulatory factor; inflammatory disorder; immune disorder; rheumatoid arthritis; lupus and graft versus host disease.
XX	
OS	Homo sapiens.
XX	
PN	WO200047740-A2.
XX	
PD	17-AUG-2000.
XX	
PF	11-FEB-2000; 2000WO-US03653.
XX	
PR	12-FEB-1999; 99US-0119906.
PR	18-NOV-1999; 99US-0166271.
XX	
PA	(AMGE-) AMGEN INC.
XX	

PI	Boyle WJ, Hsu H:
XX	
DR	WPI: 2000-556217/51.
XX	
Pt	Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g. rheumatoid arthritis -
PS	Claim 14; Fig 9; 71pp; English.
XX	
CC	AAB08265-83 represent tumour necrosis factor (TNF) ligands. The specification describes an AGP-3 polypeptide, which is TNF ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulin produced.
CC	AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, e.g. rheumatoid arthritis,
CC	Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic acids are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3-related proteins.
CC	
CC	
CC	
SQ	Sequence 160 AA;
OY	Query Match 39.7%; Score 180.5; DB 21; Length 160; Best Local Similarity 59.7%; Pred.No. 8.7e-15; Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
Db	15 IPSIHEAHKRTSLSSWKHDQMANVSNMTFSNGKLRYK--GITYRNADICSHRVTSAQL 72 : : 18 IPSGS---HKVSLSSWMYHRCGWAKISNMTFSNGKLIVNDGFYYLVANICFRHHETSGDL 74
OY	73 TLDDPL 79 :
Db	75 ATEYL 81
RESULT 5	
ID	AAU86148 standard; Protein: 244 AA.
AC	AAU86148;
DT	15-JUL-2002 (first entry)
DE	Human PRO206 polypeptide.
KW	Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelec disorder; inflammatory disorder; immune disorder; angiogenic disorder; cyostatic; neuroprotective.
OS	Homo sapiens.
PN	WO200153486-A1.
PD	26-JUL-2001.
PF	11-FEB-2000; 2000WO-USO3565.
PR	08-MAR-1999; 99WO-USO5028. 11-MAR-1999; 99US-123972P. 11-MAY-1999; 99US-133459P. 02-JUN-1999; 99WO-US1225Z. 22-JUN-1999; 99US-140650P. 22-JUN-1999; 99US-140653P. 20-JUL-1999; 99US-144758P. 26-JUL-1999; 99US-145698P. 28-JUL-1999; 99US-146222P. 17-AUG-1999; 99US-149395P. 31-AUG-1999; 99US-151689P. 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan RJ,
 PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM,
 PI Watanabe CK, Wood WT;
 XX WPI: 2002-205567/26.
 DR N-PSDB; ABK40274.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for
 PT treating benign or malignant tumours, leukaemias and lymphoid
 PT malignancies, inflammatory, angiogenic and immunologic disorders -
 XX
 PS Claim 61; Fig 42; 302pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,
 CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
 CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
 CC macrophagal, stromal and blastocoeleic disorders, inflammatory, immune
 CC and angiogenic disorders. The polynucleotide sequences are also
 CC useful in gene therapy. AA086128-AA086162 represent the human PRO
 CC polypeptides of the invention.
 XX
 SO Sequence 244 AA;
 Query Match 39.7%; Score 180.5; DB 23; Length 244;
 Best Local Similarity 59.7%; Pred. No. 1.5e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 OY 15 IPSISHEAKRTSLSSWKHDQMANVSNMTFSNGKLRV--GIYYRADICSRHRTVSAGL 72
 DB 102 IPSGS---HKVSLSSWYHDGMAKISNMFTSNGKLIYNODGFYLVANICFRHHTSGDL 158
 OY 73 TLQDQL 79
 DB 159 ATEYLQL 165
 XX
 RESULT 6
 AAU78286
 ID AAU78286 standard; Protein; 244 AA.
 XX
 AC AAU78286;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human TRANCE protein splice variant 2.
 XX
 KW Human: tumour necrosis factor-related activation induced cytokine;
 KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
 KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
 KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
 KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
 KW cartilage growth; skeletal growth.
 XX
 OS Homo sapiens.
 XX
 PN WO200216551-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 20-AUG-2001; 2001WO-US26101.
 XX
 PR 18-AUG-2000; 2000US-226197P.

XX
 PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
 XX
 PI Choi Y, Odgren PR, Marks SC;
 XX
 DR WPI: 2002-304119/34.
 DR N-PSDB; ABK12877.
 XX
 PT Treating mammal having disorder characterised by abnormal
 PT cartilage/skeletal growth such as dwarfism, acromegaly, by
 PT administering tumour necrosis factor-related activation induced
 PT cytokine-modulating agent to mammal -
 XX
 PS Disclosure; Fig 4; 55pp; English.
 XX
 CC The present invention relates to a new method of treating a mammal
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth. The method of the invention involves administering to
 CC the mammal a tumour necrosis factor-related activation induced cytokine
 CC (TRANCE)-modulating agent. The method is useful for treating a mammal
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth, where the disorder comprising insufficient cartilage or
 CC skeletal growth is selected from dwarfism, osteopetrosis,
 CC craniofacial-skeletal discrepancies and bone or cartilage damage
 CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
 CC arthritis, and disorders comprising excessive cartilage or skeletal
 CC growth are selected from acromegaly, gigantism, exostosis, cartilage,
 CC exostosis bursata and multiple osteocartilaginous exostoses. The method
 CC is useful for inhibiting chondrocyte differentiation. The present amino
 CC acid sequence represents the human TRANCE protein, splice variant 2, of
 CC the invention. TRANCE is a member of the tumour necrosis factor family
 CC and acts directly on cartilage-producing cells (chondrocytes).
 XX
 SO Sequence 244 AA;
 Query Match 39.7%; Score 180.5; DB 23; Length 244;
 Best Local Similarity 59.7%; Pred. No. 1.5e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 OY 15 IPSISHEAKRTSLSSWKHDQMANVSNMTFSNGKLRV--GIYYRADICSRHRTVSAGL 72
 DB 102 IPSGS---HKVSLSSWYHDGMAKISNMFTSNGKLIYNODGFYLVANICFRHHTSGDL 158
 OY 73 TLQDQL 79
 DB 159 ATEYLQL 165
 XX
 RESULT 7
 AAW83020
 ID AAW83020 standard; Protein; 246 AA.
 XX
 AC AAW83020;
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX
 KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.

12-AUG-1997; 97JP-0217897.
PR 21-AUG-1997; 97JP-0224803.
XX
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI: 1998-594563/50.
DR N-PSDB; AAV69899.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
XX
XX
XX Example 28; Pages 119-120; 151pp; Japanese.
XX
XX
XX The present sequence represents an osteoclastogenesis inhibitory factor
CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC separation and maturation of osteoclasts in the presence of bone
CC absorption factors such as calcitriol or parathyroid hormone (PTH).
CC OBM is isolated from stroma cells cultured in the presence of a bone
CC absorption factor by separation and solubilisation of membrane proteins
CC then affinity chromatography using OCIF. It exists in a full-sequence
CC form and a solubilised form (sOBM) which is a shorter chain. OBM may be
CC used for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
XX components of drugs.
XX
XX Sequence 246 AA:

[illegible]

PR 23-JUN-1997; 97US-0880855.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ;
XX
DR WPI; 1998-594578/50.
DR N-PSDB; AAV70285.
XX
PT Nucleic acid encoding osteopontin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
XX and for diagnosis
XX
PS Claim 19; Fig 4; 47pp; English.
XX

The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotegerin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of oeg binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteopetrosis, loosening of prostheses, optionally in combination with agents that promote bone growth.

SQ	sequence	317 AA;
	Query Match	39.7%; Score 180.5; DB 19; Length 317;
	Best Local Similarity	59.7%; Pred. No. 2.le-14;
	Matches 40; Conservative	4; Mismatches 18; Indels 5; Gaps 2;
OY	15 IPSISHEAHKRTSLSSMKHDOOMANVSNMTEFSGKLRYK--GIYYRNADICSRHRYTSAGL 72 : 175 IPFGS---HKVSLSWYHDRCMAKISMNMTFSNGKLIIVMODGFYYLYANICFRHHETSGDL 231	
OY	73 TLQDLOL 79 :	
Db	232 ATEYLQL 238	
RESULT 9		
ID	AAM83018 standard; Protein; 317 AA.	
XX	AAM83018;	
DT	10-FEB-1999 (first entry)	
DE	Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).	
KW	Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism; human.	
OS	Homo sapiens.	
PJ	MO8846644-AI.	
PD	22-OCT-1998.	
PF	15-APR-1998; 98WO-JP01728.	
PR	02-DEC-1997; 97JP-0332241.	

```

PR      15-APR-1997;    97JP--0097808.
PR      09-JUN-1997;    97JP--0151434.
PR      12-AUG-1997;    97JP--0217897.
PR      21-AUG-1997;    97JP--0224803.
PA      (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI      Goto M., Higashio K., Kinoshaki M., Kobayashi F., Morinaga T.;
PI      Nakagawa N., Shima N., Takahashi K., Tomoyasu A., Tsuda E.;
PI      Washida N., Yamaguchi K., Yano K., Yasuda H.;
XX
DR      WPI: 1998-594563/50.
DR      N-PSDB; AAV69887.
XX
PT      Protein binding to osteoclastogenesis inhibitory factor - useful
PT      for, e.g. treatment and investigation of disorders of bone and
PT      calcium metabolism
XX
PS      Claim 36; Pages 113-114; 151pp; Japanese.
XX
CC      The present sequence represents an osteoclastogenesis inhibitory factor
CC      (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC      separation and maturation of osteoclasts in the presence of bone
CC      absorption factors such as calcitriol or parathyroid hormone (PTH).
CC      OBM is isolated from stroma cells cultured in the presence of a bone
CC      absorption factor by separation and solubilisation of membrane proteins
CC      then affinity chromatography using OCIF. It exists in a full-sequence
CC      form and a solubilised form (sOBM) which is a shorter chain. OBM may be
CC      used for screening potential inhibitors and modifiers of its biological
CC      activity, and screening for receptors to OBM which mediate its function.
CC      These substances can then be used in the treatment of disorders of bone
CC      function and calcium metabolism. The antibodies can be used for assay
CC      components of drugs.
CC
SQ      Sequence     317 AA;
XX
Query Match          39.7%; Score 180.5; DB 19; Length 317;
Best Local Similarity 59.7%; Pred. No. 2.1e-14;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
OY      15 IPSISHEAKHTSLSSMKHDODMANVSNMFNSGKLRYK--GIYYRNADICSRHYTSAGL 72
Db      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
        : |||
QY      73 TLQDLQL 79
Db      232 ATGYLQL 238
RESULT 10
AAW69957
ID      AAW69957 standard; Protein; 317 AA.
XX
CC      AAW69957;
XX
DT      08-OCT-1998 (first entry)
XX
DE      NF-kB receptor activator RANK ligand (RANKL).
XX
KW      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW      immune response; inflammatory response; toxic shock; sepsis;
KW      RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
OS      Homo sapiens.
XX
PN      WO9828426-A2.
PD
PD      02-JUL-1998.
PF      22-DEC-1997;    97WO-US23775.
PR      14-OCT-1997;    97US-0064671.

```

PR	23 -DEC-1996;	96US--0059978.
PR	07 -MAR-1997;	97US--0813509.
PA	(IMMV) IMMUNEX CORP.	
PI	Anderson DM, Galibert LJ, Maraskovsky E;	
DR	N-PSDB; AAV41378.	
PT	New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells	
PS	Claim 27; Pages 59-60; 80pp; English.	
CC	This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-KB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-KB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug screening.	
SQ	Sequence 317 AA:	
Query Match	39.7%; Score 180.5; DB 19; Length 317;	
Best Local Similarity	59.7%; Pred. No. 2,le-14;	
Matches 40; Conservative 4;	Mismatches 16; Indels 5; Gaps 2	
OY	15 IPSISHEAHKTSLSWKHDDQANVSNMFTSGKLRVK--GIYYRNADICSRHRTSAGL 72 : I P S G S -- H K V S L S W Y H D R G W A K I S N M F T S G K L I V N Q D G F Y U Y L A N I C F R H H E T S G D L 231	
Db	175 IPSSGS--HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFUYLYLANICFRHHETSGL 231	
OY	73 TLQDQL 79 :	
Db	232 ATLEYDL 238	
RESULT 11		
AAM68293		
ID	AAM68293 standard; Protein; 317 AA.	
XX	AAW68293;	
AC		
DT	08-OCT-1998 (first entry)	
DE	NF-kB receptor activator RANK ligand (RANKL).	
KX	RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;	
KW	immune response; inflammatory response; toxic shock; sepsis;	
KM	RANKL; RANK ligand; tumour necrosis factor; TNF.	
XX		
OS	Homo sapiens.	
PN	W09828424-A2.	
FD	02-JUL-1998.	
PF	22-DEC-1997; 97WO-U523866.	

XX 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.

PA (IMMUNEX) IMMUNEX CORP.

PI Anderson DM, Galibert LJ, Maraskovsky E;

DR WPI: 1998-377655/32.

DR N-PSDB: AAV41372.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis

PS Example 7; Pages 59-60; 80pp; English.

XX This represents a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-KB) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 317 AA:

Query Match 39.7%; Score 180.5; DB 19; Length 317;
 Best Local Similarity 59.7%; Pred. No. 2.1e-14;

Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKHTSLSSWKHDODANVSNMFTSNGKLRVK--GIYYRNADICSRHRYT\$AGL 72
 DB 175 IPGSG---HKVSLSSWYHGRMAKISNMFTSNGKLIYNODGFYLLANICFRHHTSGDL 231

QY 73 TLQDLQL 79
 DB 232 ATEYLQL 238

RESULT 12

ID AAY84417 standard; Protein; 317 AA.

AC AAY84417;

DT 25-JUL-2000 (first entry)

XX Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 49..69

FT Domain /note="transmembrane region"

FT Region /note="extracellular stalk domain"

FT Region /note="active ligand moiety"

XX WO200015807-A1.

XX 23-MAR-2000.

XX 13-SEP-1999; 99WO-DK00481.

XX 15-SEP-1998; 98DK-0001164.

XX 02-OCT-1998; 98US-0102896.

XX (MEBT-) M & E BIOTECH AS.

PI Halkier T, Haaning J;

DR WPI: 2000-271444/23.

DR N-PSDB: AAZ99964.

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -

PS Claim 19; Page 78-79; 110pp; English.

XX The present sequence represents a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 317 AA:

Query Match 39.7%; Score 180.5; DB 21; Length 317;
 Best Local Similarity 59.7%; Pred. No. 2.1e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKHTSLSSWKHDODANVSNMFTSNGKLRVK--GIYYRNADICSRHRYT\$AGL 72
 DB 175 IPGSG---HKVSLSSWYHGRMAKISNMFTSNGKLIYNODGFYLLANICFRHHTSGDL 231

QY 73 TLQDLQL 79
 DB 232 ATEYLQL 238

RESULT 13

ID AAE08738 standard; Protein; 317 AA.

AC AAE08738;

DT 15-NOV-2001 (first entry)

XX Human receptor activator of NF kappaB ligand (RANKL) protein.

XX Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX Homo sapiens.

XX US6271349-B1.

XX 07-AUG-2001.

31-JUL-2001 (first entry)

Human full-length RANKL (receptor activator of NF-kappaB ligand).

Human: receptor activator of NF-kappaB; RANK: nuclear factor-kappaB; NF-kappaB: tumour necrosis factor; TNF: type I transmembrane protein; TNF receptor-associated factor; TRAF: RANK ligand; RANKL: osteopontin; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; EDO; early onset Paget's disease of bone; BP: cytotactin; chromosome 13q14

Homo sapiens.

WO200136637-A1.

25-MAY-2001.

14-NOV-2000; 2000WO-US31459.

17-NOV-1999; 99US-0442029

(IMMV) IMMUNEX CORP.

Anderson DM, Hughes AE,

WPI; 2001-329222/34.

N-PSDB; AAD05904.

New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -

Disclosure; Page 76-77; 96pp; English.

The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor-associated factors (TRAFs). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene activating mutations, associated with e.g. familial expansile osteolysis (FEO), and early onset Paget's disease of bone (EP). The present amino acid sequence is full-length human RANKL (huRANKL) protein. The RANKL gene is located in chromosome 13q14.

SQ **Sequence** **317 AA;**

Query Match	Score	DB	Length
39.78;	180.5;	22;	317;

Matches	40;	Conservative	4;	Mismatches	18;	Indels	5;	Gaps	2;
---------	-----	--------------	----	------------	-----	--------	----	------	----

OY 15 IPSLSHEAHTSLSSMKHDODANVANSTFNSCKLRVK--GIYYRADICSHRVTSAGL 72
||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 175 IPGS--HKVSLSSMYHDCRAKISNNTFSNGKLIVNDGFYLYLANICFRHHETSDDL 231

QY	73	TLQDLQ	79
		:	
Db	232	ATEYLQ	238

1
2
3

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:16:58 ; Search time 450.782 Seconds
(without alignments)
7329.213 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204
Sequence: 1 catgagctcataaacgag.....gtaattgagatcatcac 204

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_esthu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_huv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.6	46.4	659	17	AG107545 Pan trogl
2	84	41.2	612	17	BH267783 CH230-186
3	46.2	22.6	362	10	AV653073 AV653073
4	33.8	16.5	284	17	AL768846 AL768846
5	33.6	16.3	530	9	AA310614 AA310614
6	33.2	16.3	853	17	BH314331 BH314331

7	32.8	16.1	407	10	AW750032	AW750032	PM2-BT054
8	32.8	16.1	561	10	AV979271	AV979271	AV979271
9	32.8	16.1	724	17	BH671765	BH671765	BH671765
10	32.4	15.9	823	17	CNS05974	CNS05974	CNS05974
11	32.4	15.9	1027	14	BQ050697	BQ050697	BQ050697
12	32.2	15.8	771	17	A2724950	A2724950	APCI-24-6
13	32	15.7	463	12	BF930674	BF930674	BF930674
14	32	15.7	912	12	BF683775	BF683775	BF683775
15	31.8	15.6	428	9	AU265504	AU265504	AU265504
16	31.6	15.5	426	17	AQ532546	AQ532546	HS-5207_A
17	31.6	15.5	451	13	BQ445420	BQ445420	BQ445420
18	31.4	15.4	341	10	AW784685	AW784685	AW784685
19	31.4	15.4	704	9	A1896022	A1896022	EST265465
20	31.4	15.4	1074	17	CNS04422F	CNS04422F	CNS04422F
21	31.2	15.3	306	9	AA188893	AA188893	zp/9a11.r
22	31.2	15.3	483	10	AW750034	AW750034	AW750034
23	31.2	15.3	493	10	AW959012	AW959012	AW959012
24	31.2	15.3	517	10	B1260179	B1260179	EST371082
25	31.2	15.3	545	13	BM836932	BM836932	K-EST0112
26	31.2	15.3	558	14	AM958677	AM958677	EST370747
27	31.2	15.3	646	10	AM814742	AM814742	MR1-S7020
28	31.2	15.3	694	10	AC013309	AC013309	AC013309
29	31.2	15.3	698	17	AC013309	AC013309	AC013309
30	31.2	15.3	701	12	BG768911	BG768911	BG768911
31	31.2	15.3	728	12	BG761703	BG761703	602718992
32	31.2	15.3	729	12	BG422303	BG422303	602448955
33	31.2	15.3	743	12	BG284886	BG284886	602409121
34	31.2	15.3	792	13	BM044745	BM044745	603622491
35	31.2	15.3	819	17	BH419036	BH419036	BOGVM75TR
36	31.2	15.3	836	17	BH505193	BH505193	BOGNE22TF
37	31.2	15.3	844	14	BO895831	BO895831	AGENCOURT
38	31.2	15.3	847	14	BO900660	BO900660	AGENCOURT
39	31.2	15.3	871	14	BO935750	BO935750	AGENCOURT
40	31.2	15.3	907	14	BQ220873	BQ220873	AGENCOURT
41	31.2	15.3	910	14	BQ918817	BQ918817	AGENCOURT
42	31.2	15.3	916	14	BE542870	BE542870	601677690
43	31.2	15.3	941	12	BE782157	BE782157	601467760
44	31.2	15.3	959	14	BO894167	BO894167	AGENCOURT
45	31.2	15.3	974	14	BQ053094	BQ053094	AGENCOURT

ALIGNMENTS

RESULT 1
AG107545 659 bp DNA linear GSS 03-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-112609.F, genomic survey sequence.
DEFINITION AG107545
ACCESSION AG107545
VERSION GI:16728063
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes male lymphoblast DNA, clone: PTB Chimpanzee Male
BAC library clone: PTB-112609.F.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC and sequences of library PTB
Unpublished
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hnp.gsc.riken.go.jp/)
Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.

COMMENT

JOURNAL

PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. .659
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PMB-112609.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 181 a 168 c 121 g 189 t
ORIGIN

Query Match
Best Local Similarity 74.9%; Score 94.6; DB 17; Length 659;
Matches 134; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 8 CTCATTAAGAGCTCTTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTCCACA 67
DB 410 CCCATTAAGAGCTCTTCTTCTTGGTACCATGATGGGGTTGGCCAGATCTCCACA 469
QY 68 TGACTTTAGCAAGGAAACTAAGTCA-----AAGCATTTATTAACCGGAATGCCG 121
DB 470 TGACTTTAGCAAGGAAACTAAGTCAAGGATGGCTTTATTAATCTGTATGCCA 529
QY 122 ACATTGCTCTGACATCGCTGACGAGCCTTAACCTGCGAGGACCTTCAAGCTA 180
DB 530 ACATTGCTCTGACATCATGAACTTCAGAGACCTTGTACAGATATATCTTCAACTA 588

RESULT 2
BH267783/c
LOCUS BH267783 612 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-186C1, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION CH230-186C1, DNA sequence.
VERSION BH267783
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 612)
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, U., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
COMMENT Other:SSS: CH230-186C1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_eirng_information.htm). BAC end
plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .612
/organism="Rattus norvegicus"

FEATURES
source

1. .612
/organism="Rattus norvegicus"

/strain="BN/SSnHsd/MCw"
/db_xref="taxon:10116"
/clone="CH230-186C1"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SSnHsd/MCw) BAC library produced by
Pieter de Jong"

BASE COUNT 168 a 145 c 133 g 166 t
ORIGIN

Query Match
Best Local Similarity 71.3%; Score 84; DB 17; Length 612;
Matches 127; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

QY 8 CTCATTAAGAGCTCTTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTCCACA 67
DB 591 CCCATTAAGAGCTCTTCTTCTTGGTACCATGATGGGGTTGGCCAGATCTCCACA 532
QY 68 TGACTTTAGCAAGGAAACTAAGTCA-----AAGCATTTATTAACCGGAATGCCG 121
DB 531 TGACTTTAGCAAGGAAACTAAGGTTTACCAAGATGGCTTATTAATCTGTATGCCA 472
QY 122 ACATTGCTCTGACATCGCTGACGAGCCTTAACCTGCGAGGACCTTCAAGCTA 179
DB 471 ACATTGCTCTGACATCATGAACTTCAGAGACCTTGTACAGATATATCTTCAACTA 414

RESULT 3
AV653073
LOCUS AV653073 362 bp mRNA linear EST 15-JAN-2002
DEFINITION AV653073 GLC Homo sapiens cDNA clone GLCDB01.3, mRNA sequence.
ACCESSION AV653073
VERSION AV653073.1 GI:9874087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 362)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Gu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. .362
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCDB01"
/clone_lib="GLC"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_nos="SOLR"
/note="Vector: pBluescript sk(-); Site 1: EcoRI; Site 2:
XhoI"

BASE COUNT 102 a 80 c 78 g 100 t 2 others
ORIGIN

Query Match

22.6%; Score 46.2; DB 10; Length 362;

9 TCATAAACGAGTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTCCAAGAT 68

QY 11 ATAAACGAGTCTTCTCTTGGAAACATGACCAGATTGGCAACCTCTCCACATGA 70
 | | | | | | | | | | | | | | | | | | | | | |
 385 ATACACCTGCAAGCTCCAGAAATGCTGCCCAAGTGGAGAGAGACTTNAAGGCACGA 344

OY 71 CTTGACGACGAGAACTAGAGTCAGGCAATTTATACGGAGTGGCAGATT 126
 Db 345 NTTAAATGTGGGACAGGACATTCAGGCAATTTATGTAATNGGAGAAATT 400

RESULT 6
 BH314331
 LOCUS

DEFINITION BH314331 853 bp DNA linear GSS 03-DEC-2001
 CH230-99C2, IV CHORI-230 Segment 1 Rattus norvegicus genomic clone

ACCESSION BH314331
 VERSION BH314331.1 GI:17244682
 KEYWORDS GSS.

SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 853)

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
 A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, P., de
 Jong, P. and Fraser, C. M.

TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment.
 JOURNAL Unpublished (1999)
 COMMENT Other GSS: CH230-99C2.TU

Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@tigr.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ordering information.htm). BAC end
 plates: 99 row: C column: 2
 Seq primer: 77
 Class: BAC ends.
 Location/Qualifiers

FEATURES
 source 1..853

/organism="Rattus norvegicus"
 /strain="BN/SSNHSd/MCM"
 /db_xref="taxon:10116"
 /clone="CH230-99C2"
 /clone_lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
 CHORI-230 Rat (BN/SSNHSd/MCM) BAC library produced by
 Pieter de Jong"

BASE COUNT 302 a 190 c 184 g 177 t

Query Match 16.3%; Score 33.2; DB 17; Length 853;
 Best Local Similarity 53.0%; Pred. No. 1.8;
 Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

OY 2 ATGAGGCTCAATAAAGCGCTTCTTCTTGGAAACATGACCAAGATGGGCAACGCT 61
 Db 430 ATGAAATTCATAGCAAAATGCTTGGAAACATGACCAAGATGGGCAACGCT 489
 OY 62 CCAACATGATCTTGGCAAGCAAACTAAGAGTCAAGGCAATTTATACCGGAATGCG 121
 Db 490 CCAAGAGACATACATGATGATGCTATGCACTCATGATTAAGGCTATTAAGCCAAATGCT 549
 OY 122 ACATTTCTCTCGA 135
 Db 550 TGAATTAATCTAGA 563

RESULT 7
 AW750032
 LOCUS

DEFINITION PM2-BT0546-120100-001-a08 BT0546 Homo sapiens cDNA, mRNA sequence.
 AW750032
 VERSION AW750032.1 GI:7664964

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 407)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
 Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
 Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 JOURNAL sequence tags
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?PM2&t2=PM2-BT0546-
 120100-001-a08&t3=2000-01-12&t4=1)

Seq primer: puc 18 forward
 High quality sequence stop: 406.
 Location/Qualifiers

FEATURES
 source 1..407

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BT0546"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from OESTRES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 135 a 73 c 109 g 90 t

Query Match 16.1%; Score 32.8; DB 10; Length 407;
 Best Local Similarity 55.2%; Pred. No. 1.7;
 Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

OY 11 ATAAACGAGCTTCTTCTTGGAAACATGACCAAGATGGGCAACGCTTCAACATGA 70
 Db 258 AAACAACGAGCAACCTCCAGAAATGCTGCCAAGTGAAGAGAGTGAAGCAGCA 317
 OY 71 CTTGACGACGAGAACTAAGAGTCAAGGCAATTTATACCGGAATGCGCAAT 126
 Db 318 ATGAAATGTGGGACAGGACAGGACATTCAGGCAATTTATGTAATGCGCAGACAT 373

RESULT 8
 AV979271
 LOCUS

DEFINITION AV979271 561 bp mRNA linear EST 14-MAR-2002
 intestinalis cDNA clone cleg52120 5', mRNA sequence.
 ACCESSION AV979271
 VERSION AV979271.1 GI:19468995

KEYWORDS EST.

SOURCE	Clona intestinalis.
ORGANISM	Clona intestinalis
REFERENCE	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cloniidae; Clona.
AUTHORS	I (bases 1 to 561)
TITLE	Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
JOURNAL	Expressed genes in Clona intestinalis Unpublished (2000) Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel.: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp.
COMMENT	Location/Qualifiers
FEATURES	1..561
SOURCE	/organism="Clona intestinalis" /db_xref="taxon:7219" /cdone="cleg52120" /clone_id="Nori Satoh unpublished cDNA library, egg" /tissue_type="whole animal" /dev_stage="egg" /note="vector: pBluescript SK"
BASE COUNT	150 a 127 c 127 g 157 t
ORIGIN	
Query Match	16.1%; Score 32.8; DB 10; Length 561;
Best Local Similarity	51.4%; Pred. No. 2;
Matches	76; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
OY	12 TAAACGAGCTTTTCTTCTTGGAACATGACCACATGTGGCGAAGCCTCCACATGCAC 71
DB	228 TCAAACCAACACACTGGCTGGTTAACTCAGAACAATTGAGAAATGCCACACCTGGGAC 287
OY	72 TTTCACCAACGGGAAAATAAGAGTCAAAGCATTTATTATACCGGAATGCCGACATTTGCTC 131
DB	288 TTATATACACGGAGACATTAAGGAGAAAGCATCCOACACTCTGTGATGCATGCTTTG 347
OY	132 TCGACATCGGTAACTCAGCAGGCGCTA 159
DB	348 AAGACCAAGAGAAAGCTGTATGCTTA 375
RESULT 9	
BH671765/c	724 bp DNA linear GSS 19-FEB-2002
LOCUS	BOMKJ36TR BO_2-3_KB Brassica oleracea genomic clone BOMK36, DNA
DEFINITION	sequence.
ACCESSION	BH671765
VERSION	BH671765.1 GI:18736884
KEYWORDS	GSS.
SOURCE	Brassica oleracea.
ORGANISM	Brassica oleracea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 724) Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea unpublished (2001) Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Class: sheared ends. Location/Qualifiers 1..724 /organism="Brassica oleracea"
FEATURES	
SOURCE	

[illegible]

RESULT 10	823 bp	DNA	linear	GSS 26-MAY-2000
CNS05RMX/c				
LOCUS				
DEFINITION	CNS05RMX	Tetraodon nigroviridis genome survey sequence SP6 end of clone 004K23 of library B from Tetraodon nigroviridis, genomic survey sequence.		
ACCESSION	AL350754	GI:8244524		
VERSION	AL350754.1	GI:8244524		
KEYWORDS	GSS; genome survey sequence.			
SOURCE	Tetraodon nigroviridis.			
ORGANISM	Tetraodon nigroviridis			
REFERENCE	1 (bases 1 to 823)			
AUTHORS	Roest-Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.			
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 823)			
AUTHORS	Roest-Crolius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.			
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 823)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-APR-2000)			
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .			
FEATURES	Location/Qualifiers			
SOURCE	1..823			
	/organism="Tetraodon nigroviridis"			
	/db_xref="taxon:99883"			
	/clone="004K23"			
	/clone_1lb="B"			
	/note="Genoscope sequence ID : COAB004F12B1-end : SP6"			
BASE COUNT	185 a 154 c 189 g 259 t 36 others			
ORIGIN				

Query Match 15.9%; Score 32.4; DB 17; Length 823;
Best Local Similarity 50.4%; Pred. No. 3.3;
Matches 63; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

OY 71 CTTTACGACGAGAACTAAGATCAAGGCAATTTATTACCGAATGCCGACATTTGCT 130
DB 731 CTTTGCNCAANANANATTAACCAANTTAACCTTTTNCACCCCAACGCGTCAGCG 672
OY 131 CTCGACATCGCGTACACCGAGCGGCTACACTGACGAGCCTTACGCTATGCTAATT 190
DB 671 CTTGACACCGTGGAGAGTGAAGACACACACACACACACACACACACACACACAC 612
OY 191 TGAGA 195
DB 611 TGANA 607

RESULT 11
B0050697/c
LOCUS 1027 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6808690 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784700
ACCESSION B0050697
VERSION B0050697.1 GI:19810037
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1027)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12870 row: k column: 05
High quality sequence stop: 642.

FEATURES
Source Location/Qualifiers

1..1027
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5784700"
/clone_lib="NIH_MGC_71"
/tissue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
BASE COUNT 286 a 233 c 214 g 292 t 2 others
ORIGIN

Query Match 15.9%; Score 32.4; DB 14; Length 1027;
Best Local Similarity 53.7%; Pred. No. 3.7;
Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 9 TCATAAACGAGCTCTTCTTCTTGAACATGACCAAGATTGGGCAACGCTCCACAT 68
DB 688 TCAAAATAAAGTTTATTTTGAATAAAGTGTATTAAGTTTGAACAAAGTNTAAACA 629
OY 69 GACTTTCAGCAACGAAACTAAGATCAAGGCAATTTATTACCGAATGCCGACATTTG 128
DB 628 TTTTCTTCTTCTTGAAGAAAGTAAATCTGAAGAAGTAATTCATTATCAATACATCAG 569
OY 129 CTC 131
DB 568 CTC 566

RESULT 12
A2724950
LOCUS 771 bp DNA linear GSS 24-JAN-2001
DEFINITION RPCI-24-64B19.TJ RPCI-24 Mus musculus genomic clone RPCI-24-64B19,
DNA sequence.
ACCESSION A2724950
VERSION A2724950.1 GI:12471113
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 771)
Zhao S., Nietman, W., Malek, J., Shatsman, S., Aklnet, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
JOURNAL Mouse BAC End Sequences from Library RPCI-24
COMMENT Unpublished (1999)
Other GSSs: RPCI-24-64B19.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPC
Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
plate: 64 row: B column: 19
Seq primer: SP6
Class: BAC ends.

FEATURES
Source Location/Qualifiers

1..771
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-64B19"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTRABAC1; Site: 1; BamHI; Site: 2; BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTRABAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."
BASE COUNT 331 a 110 c 131 g 199 t
ORIGIN

Query Match 15.8%; Score 32.2; DB 17; Length 771;
Best Local Similarity 52.6%; Pred. No. 3.8;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

OY 28 TCTTGAACATGACCAAGATTGGGCAACGCTCCACATGACTTTCAGCAACGGAAGA 87
DB 199 TTTTGAAGATTAAGAGATTGACCAATCTCAGCAACATCAAGGAGAAAGAAAG 258
OY 88 CTAAAGCTCAAGGATTTATTACCGAATGCCGACATTTGCTTCGACATCGCTAAC 147
DB 259 ATCCAAATCAATACGCTTATGATCAAAAGAGAGCCATTAATAAATATTCAGGAATTC 318
OY 148 TCAGCAGGCTTAA 160
DB 319 AGTCAGGCTTAA 331

RESULT 13
BF930674
LOCUS 463 bp mRNA linear EST 22-JAN-2001

DEFINITION MR2-NT0135-131200-014-901 NT0135 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BF930674
 VERSION BF930674.1 GI:12347907
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 463)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brienes,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 2020263
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&tl2=MR2-NT0135-131200-014-901&tl3=2000-12-13&tl4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 462.
 Location/Qualifiers
 1..463
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NT0135"
 /dev_stage="Adult"
 /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 156 a 97 c 115 g 95 t
 ORIGIN
 Query Match 15.7%; Score 32; DB 12; Length 463;
 Best Local Similarity 56.7%; Pred. No. 3.5;
 Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 CATGAGGCTCATTAACGAGCTCTTCTTGGAACATGACCAAGATTGGCCAAACGTC 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 64 CACGAGAGAGACACGACGAGAGAGCTCTTCTTGGAACATTAACGAGAAATGCGAAAGCGCT 123
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 TCCACATGATCTTTCAGCAGCAAGCAAACTAAGATCAAGGCAAT 104
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 124 TGCAGCAGCTACAGAGAGATTCAGAAATTAAGACCAAGCCTT 167
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 14
 BF683775 912 bp mRNA linear EST 22-DEC-2000
 LOCUS 60214005891 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301127 5',
 DEFINITION mRNA sequence.
 ACCESSION BF683775
 VERSION BF683775.1 GI:11969183
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 912)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LICM1161 row: C column: 16
 High quality sequence stop: 720.
 Location/Qualifiers
 1..912
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:4301127"
 /clone_lib="NIH_MGC_46"
 /tissue_type="Telomysarcoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 BASE COUNT 295 a 181 c 258 g 178 t
 ORIGIN
 Query Match 15.7%; Score 32; DB 12; Length 912;
 Best Local Similarity 50.0%; Pred. No. 4.8;
 Matches 80; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
 QY 11 ATTAACGAGTCTTTCTTGTGGAACATGACCAAGATTGGCAACGCTCCACATGA 70
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 361 AAACAACGAGCCACGCTCCAGAAAATGCTGCCACCTCGAAGAGTTGAAGGACGA 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 71 CTTTCGACGCAAGCAAACTAAGATCAAGGCTTATTACCGGATGCGGACATTTGCT 130
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 421 ATTGAATTGTGGACAGCAAGACATTTCAAGGCTTTATGTGTAATGGCAGAAATTCATG 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 131 CTGACATCGCGTAACTCAGCAGGCTTAACCTTGCGAGA 170
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 481 GAGTATGTGCGAGAACATGAGATGATCATGATGAGAA 520
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 15
 AU226504 428 bp mRNA linear EST 23-APR-2002
 LOCUS AU226504 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-39-G24 3',
 DEFINITION mRNA sequence.
 ACCESSION AU226504
 VERSION AU226504.1 GI:19741151
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 428)
 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arikawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
 Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)

COMMENT

Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel.: 81-298-36-4350
Fax: 81-298-36-9060
Email: msek@rctc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda PTC-1 vector (Garnica et al., submitted for publication), digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for further details.

FEATURES

URES	Location/Qualifiers
source	1. .428

```
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/colloc="par14-30_034"
```

```
/clone="RAFL14-39-G24"
/clone lib="RAFL14"
```

```
/clone_lib="RAFL14"
/tissue_type="root"
```

```
/c/lssue_type="root"  
/lab_host="DH10B"
```

```
/rad_host- DnaB
/note="Site_1: BamHI;
```

	92 c	73 g	123 t
a			

BASE COUNT ORIGIN	140 a	92 c	73 g	123 t
----------------------	-------	------	------	-------

ORIGIN

Query Match	Score	DB	Length
15.68;	31.8;	9;	428;
Best Local Similarity	54.89;	Best	428;

Best Local Similarity 54.8%; Pred. NO. 4;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

15 AACGAGTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCCAACATGACTTT 74

Db 16 AATGGTCTTCTTAATAATCAACAATCACATGACATGACCAACAAGTGTGATT 75

QY 75 CAGCAACGAAACTAAGAGTCAAGGCATTATTACCGGAATGCCGACATTTC 129

Db 76 CAGAGAGATATCTCAGAGTTTAAAGGAATATTAACTCATTTACGATTGTTTC 130

Search completed: December 8, 2002, 19:27:16
Job time : 459.782 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:14 ; Search time 58.0886 Seconds
(without alignments)
7908.746 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204
Sequence: 1 catgagcctcataaacgag.....gtatttgagatcattcac 204

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	95.1	1186	24	ABK33576
2	96.4	47.3	741	19	AAV69889
3	96.4	47.3	954	19	AAV69887
4	96.4	47.3	954	19	AAV1376
5	96.4	47.3	954	19	AAV1372
6	96.4	47.3	954	22	AAV15311
7	96.4	47.3	954	22	AAV08715
8	96.4	47.3	954	22	AAV05904
9	96.4	47.3	1945	24	ABK12877

10	96.4	47.3	2226	24	ABK12876
11	96.4	47.3	2271	21	AAZ99964
12	96.4	47.3	2274	19	AAV70285
13	96.4	47.3	2390	24	ABK40274
14	93.2	45.7	1823	20	AAV80223
15	84	41.2	957	22	AAV68481
16	80.8	39.6	735	19	AAV69898
17	80.8	39.6	951	21	AAV69900
18	80.8	39.6	951	21	AAV6985
19	80.8	39.6	951	21	AAV6985
20	80.8	39.6	951	21	AAV6985
21	80.8	39.6	1538	19	AAV69886
22	80.8	39.6	1574	22	AAH25526
23	80.8	39.6	1630	19	AAV41377
24	80.8	39.6	1630	19	AAV41371
25	80.8	39.6	1630	22	AAV15310
26	80.8	39.6	1630	22	AAV08714
27	80.8	39.6	1630	22	AAV08714
28	80.8	39.6	2029	21	AAV39135
29	80.8	39.6	2191	19	AAV41489
30	80.8	39.6	2237	20	AAV80224
31	80.8	39.6	2237	24	ABK12880
32	80.8	39.6	2295	19	AAV70284
33	80.8	39.6	2295	21	AAV70284
34	79.2	38.8	519	21	AAZ99968
35	61.8	30.3	519	21	AAZ99968
36	61.8	30.3	519	21	AAZ99972
37	61.8	30.3	546	21	AAZ99972
38	61.8	30.3	546	21	AAZ99970
39	61.8	30.3	564	21	AAZ99973
40	61.8	30.3	519	21	AAZ99973
41	51.2	25.1	519	21	AAZ99973
42	31.2	15.3	493	20	AAV87615
43	31.2	15.3	985	24	ABK46140
44	31.2	15.3	2276	22	ABA08774
45	31.2	15.3	3073	24	ABK46139

ALIGNMENTS

RESULT 1
ID ABR33576 standard; CDNA; 1186 BP.
AC ABR33576;
DT 08-MAY-2002 (first entry)
DE CDNA encoding human PRO protein, Seq ID No 81.
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX Homo sapiens.
OS
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220644P.
XX 25-JUL-2000; 2000US-220664P.
XX 25-JUL-2000; 2000US-220666P.
XX 26-JUL-2000; 2000US-220893P.

CDNA encoding huma
DNA encoding a hum
Human osteoprotege
CDNA encoding huma
Human TRANCE encod
Human osteoclast dif
Nucleic acid encod
Nucleotide sequenc
Mouse OBM nucleotid
DNA encoding a mur
Osteoclast formati
Nucleic acid encod
Nucleotide sequenc
NF-KB receptor act
NF-KB receptor act
Murine receptor ac
Murine RANKL (rece
Mouse OBM nucleotid
Nucleotide sequenc
Murine TRANCE enco
CDNA encoding mous
Human osteoprotege
DNA encoding a mur
Mouse CDNA encodin
DNA encoding a syn
DNA encoding a mur
DNA encoding osteo
DNA encoding osteo
DNA encoding osteo
DNA encoding osteo
EST clone D611.
CDNA encoding colo
Human cytokinesis
CDNA encoding colo

Db 438 TGCCACATTTGCTTCGACATCATGAACTTCAGAGACCTAGCTACAGATATCTTCA 497
 QY 177 GCTA 180
 111
 Db 498 ACTA 501

RESULT 3
 ID AAV69887 standard; cDNA to mRNA; 954 BP.
 AAV69887
 AC AAV69887;
 XX 10-FEB-1999 (first entry)
 DT
 XX Nucleic acid encoding a human OCIF-binding molecule (OBM).
 DE
 XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1.954
 FT CDS /tag= a

W09846644-A1.
 XX 22-OCT-1998.
 PD
 XX 15-APR-1998; 98WO-JP01728.
 PF
 XX 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.

(SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PA Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX WPI: 1998-594563/50.
 DR P-PSDB: AAM63018.

Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PS
 XX Claim 38; Page 115; 151pp; Japanese.

The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stromal cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 CC
 XX Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
 SQ
 Query Match 47.3%; Score 96.4; DB 19; Length 954;
 Best Local Similarity 74.5%; Pred. No. 2.3e-23;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
 QY 3 TGAGGCTCATTAAGAGAGCTTCTTCTTGGAAACATACCAAGTTGGGAACGCTC 62
 Db 531 TGGTTCCTCCATTAAGAGAGCTCTCTCTGGTACCATGATGGGGTGGCCAGATCTC 590
 QY 63 CAACATGACTTTCAGCAACGAAAGTAAAGTCA-----AAGCATTTATTTACCGGAA 116
 Db 591 CAACATGACTTTCAGCAACGAAAGTAAAGTCAAGTATATCATGAGATGGCTTTATTTACCTGTA 650
 QY 117 TGCCAGCATTTGCTTCGACATCATGAGACCTAGAGAGCCCTTACTCTCAGAGACTTCA 176
 Db 651 TGCCACATTTGCTTCGACATCATGAGACCTAGAGAGACCTAGAGATCTTCA 710
 QY 177 GCTA 180
 111
 Db 711 ACTA 714

RESULT 4
 ID AAV41378 standard; cDNA; 954 BP.
 AAV41378
 AC AAV41378;
 XX 08-OCT-1998 (first entry)
 DT
 XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 DE
 XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1.954
 FT CDS /tag= a
 FT /product= "human RANKL (ligand for RANK)"

W09828426-A2.
 XX 02-JUL-1998.
 PD
 XX 22-DEC-1997; 97WO-US23775.
 PF
 XX 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.

(IMMV) IMMUNEX CORP.
 XX
 PA Anderson DM, Galibert LJ, Maraskovsky E;
 PI
 PI WPI: 1998-377657/32.
 DR P-PSDB: AAM69957.

New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells
 PS
 XX Claim 25; Pages 59-60; 80pp; English.

This cDNA encodes a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANKL with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists

Db 651 TGCCACATTTGCTTCGACATCATGAAACTTCAGGAGCTAGCTACAGATATCTTCA 710
 QY 177 GCTA 180
 |||
 Db 711 ACTA 714

RESULT 8

AD05904
 ID AD05904 standard; cDNA; 954 BP.

AC AD05904;

DT 31-JUL-2001 (first entry)

DE Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.

XX Human: receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumor necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopontin;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; BP; cytostatic; chromosome 13q14;
 KW ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..954

FT /tag= a
 FT /product= "Human full-length RANKL (receptor activator
 of NF-kappaB ligand) protein"

W0200136637-A1.

25-MAY-2001.

14-NOV-2000; 2000WO-US31459.

17-NOV-1999; 99US-0442029.

(IMMUNEX CORP.

Anderson DM, Hughes AE;

WPI; 2001-329222/34.

P-PSDB; AA01993.

New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 Example 7; Page 75-76; 96pp; English.

The present invention relates to a novel receptor, referred to as RANK
 (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
 (tumor necrosis factor) receptor superfamily. RANK is a Type I
 transmembrane protein that interacts with TNF receptor-associated
 factors (TRAFs). Triggering of RANK by overexpression or co-expression
 of RANK and membrane bound NF-kappaB (RANKL) results in upregulation
 of the transcription factor NF-kappaB, a ubiquitous transcription factor
 that is most extensively utilized in cells of the immune system.
 Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
 negative effects of inflammatory reactions, and the effects of excess
 bone resorption. The RANK DNAs, proteins and their analogues are useful
 for the preparation of pharmaceutical compositions, for infecting target
 cells for use in gene therapy applications in diagnosing diseases
 associated with RANK, and as targets for use in screening assays. They
 may be used in the treatment or diagnosis of immune system dysfunction.
 The present invention also encompasses gene therapy methods to correct
 gene-activating mutations, associated with e.g. familial expansile
 osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 present sequence is a cDNA encoding full-length human RANKL (huRANKL)

CC protein. The RANKL gene is located in chromosome 13q14.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 47.3%; Score 96.4; DB 22; Length 954;
 Best Local Similarity 74.5%; Pred. No. 2.3e-23;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATATAAAGAGCTTTCTTCTTGGAAACATGACCAAGATTTGGCAACGCTTC 62

Db 531 TGGTCCCATTAAGAGATGCTCTCTTGGTACCATGATCGGCTTGGCCAAAGATCTC 590

QY 63 CAACATGACTTTGACGAACGAAACCTAAGATCA-----AAGCATTTATTTACCGGAA 116

Db 591 CAACATGACTTTTGTAGCAATGGAACCTAATAGTTAATCAGATGGCTTTTATACCTGTA 650

QY 117 TGCCGACATTTGCTCTGACATCGGTAACCTCAGCAGGCTTAACCTGACGAGACTTCA 176

Db 651 TGCCACATTTGCTTCTTGACATCATGAAACTTCAGAGACACTACAGATATCTTCA 710

QY 177 GCTA 180
 |||
 Db 711 ACTA 714

RESULT 9

ABK12877

ID ABK12877 standard; cDNA; 1945 BP.

AC ABK12877;

DT 18-JUN-2002 (first entry)

DE cDNA encoding human TRANCE protein splice variant 2.

XX Human: tumor necrosis factor-related activation induced cytokine;
 KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
 KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
 KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
 KW exostosis bursitis; multiple osteocartilaginous exostosis; chondrocyte;
 KW cartilage growth; skeletal growth; gene; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT misc_feature 81..131

FT /tag= a
 FT /note= "Tumour necrosis factor (ligand) superfamily,
 member 11 (TNFRF11), Specifically claimed in
 claim 4"

FT misc_feature 81..140
 FT /tag= b
 FT /note= "Target region for antisense nucleic acid"

FT CDS 95..829
 FT /tag= c
 FT /product= "Human TRANCE (tumor necrosis factor-related
 activation induced cytokine) protein,
 splice variant 2"

W0200216551-A2.

28-FEB-2002.

20-AUG-2001; 2001WO-US26101.

18-AUG-2000; 2000US-226197P.

(UTMA-) UNIV MASSACHUSETTS MEDICAL CENT.

Choi Y, Odgren PR, Marks SC;

WPI; 2002-304119/34.

P-PSDB; AAU78286.

XX Treating mammal having disorder characterised by abnormal
PT cartilage/skeletal growth such as dwarfism, acromegaly, by
PT administering tumour necrosis factor-related activation induced
PT cytokine-modulating agent to mammal -
XX
PS Disclosure: Fig 3; 55pp; English.
XX
XX The present invention relates to a new method of treating a mammal
CC having a disorder comprising insufficient or excessive cartilage or
CC skeletal growth. The method of the invention involves administering to
CC the mammal a tumour necrosis factor-related activation induced cytokine
CC (TRANCE)-modulating agent. The method is useful for treating a mammal
CC having a disorder comprising insufficient or excessive cartilage or
CC skeletal growth, where the disorder comprising insufficient cartilage
CC or skeletal growth is selected from dwarfism, osteopetrosis,
CC craniofacial-skeletal discrepancies and bone or cartilage damage
CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
CC arthritis, and disorders comprising excessive cartilage or skeletal
CC growth are selected from acromegaly, gigantism, exostosis, cartilage
CC exostosis bursaia and multiple osteocartilaginous exostoses. The method
CC is useful for inhibiting chondrocyte differentiation. The present
CC nucleic acid sequence encodes the human TRANCE protein, splice variant
CC 2, of the invention. TRANCE is a member of the tumour necrosis factor
CC family and acts directly on cartilage-producing cells (chondrocytes).
XX
SQ Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other:
XX
XX Query Match 47.3%; Score 96.4; DB 24; Length 1945;
Best Local Similarity 74.5%; Pred. No. 3e-23;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
OY 3 TGAGCGTCATPAAACGAGCTCTTCTCTTGGAAACATGACCAGATTTGGCAACGCTCTC 62
DB 406 TGGTTCCTCCATTAAGAGAGCTGCTCTCTTGTACATGATCGGGGTTGGCCAAAGATCTC 465
OY 63 CACATGACTTTTCGACCAACGGAACCTAAGATCA-----AAGCATTTATTACCGGAA 116
DB 466 CACATGACTTTTGGACATGGAACCACTTAATACAGATGGCTTTATTACCGTA 525
OY 117 TGGCGACATTTGCTCTGCACATCGCGTAACCTTCAGACGCTTAACCTTCGACGACTTCA 176
DB 526 TGGCAACATTTGCTTGCACATCATGAAACCTTCAGAGACTTACTACAGATGATCTTCA 585
OY 177 GCTA 180
DB 586 ACTA 589
XX
XX RESULT 10
ABK12876
ID ABK12876 standard; CDNA: 2226 BP.
XX
XX AC
XX ABK12876;
XX
XX 18-JUN-2002 (first entry)
XX
XX CDNA encoding human TRANCE protein splice variant 1.
XX
XX Human: tumour necrosis factor-related activation induced cytokine;
KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
KW exostosis bursaia; multiple osteocartilaginous exostosis; chondrocyte;
KW cartilage growth; skeletal growth; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 141..190
FT misc_feature
FT /*tag= a
FT /note= "Tumour necrosis factor (ligand) superfamily,
FT member 11 (TNFSF11), target region for antilysen

FT	CDS		157..1110 /*tag= b /product=- "human TRANCE (tumour necrosis factor-related activation induced cytokine) protein, splice variant 1"
XX		MW0200216551-A2.	nucleic acid. Specifically claimed in claim 4"
XX		28-FEB-2002.	
PD		20-AUG-2001; 2001WO-US26101.	
XX		18-AUG-2000; 2000US-226197P.	
PA	(UWMA -)	UNIV MASSACHUSETTS MEDICAL CENT.	
PX	Choi Y,	Odgren PR, Marks SC;	
XI			
DR	WIPI; 2002-304119/34.		
XX	P-PsDB; AA078285.		
PT	Treating mammal having disorder characterised by abnormal cartilage/skeletal growth such as dwarfism, acromegaly, by administering tumour necrosis factor-related activation induced cytokine-modulating agent to mammal -		
PS	Disclosure; Fig 1; 55pp; English.		
XX	The present invention relates to a new method of treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth. The method of the invention involves administering to the mammal a tumour necrosis factor-related activation induced cytokine (TRANCE)-modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or craniofacial-skeletal defects selected from dwarfism, osteopetrosis, craniofacial-skeletal dysplasias and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, carlaginae, exostosis burata and multiple osteochondrocyte differentiation. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANCE protein, splice variant 1, of the invention. TRANCE is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes).		
SQ	Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other:		
Query Match	47.3%; Score 96.4; DB 24; Length 2226;		
Best local Similarity	74.5% Pred. No. 3.2e-23;		
Matches 137; Conservative	0; Mismatches 41; Indels 6; Gaps		
OY	3 TGAGGCTCAATAAAGACGTTCCTTCTTGGAACAATGCACCAGAATTGGCGAAACTC TC 62		
Db	687 TGGTTCCCAAAAGTAGTCTCTCTCTGGTAACATCATCGGGGTGGGCAAGATCTC 746		
OY	63 CAACATGACTTCAGCACGAAAAC TAAGACTCA-----AAGGCAATTAATTACCGGAA 116		
Db	747 CAAACATGACTTTAGCAATGAGAAAAC TAATTAATTAATGAGAGTGGCTTTTATACCTGA 806		
OY	117 TGGCGACATTTGTCGTGCAGATCGGCTATCAGACAGGCTTAOCTTGCAGACCTTCA 176		
Db	807 TGGCAACATTTGCTTTCGACATCATGAACCTTCAGAGAGCCAGTCAAGAGTATCTTCA 866		
OY	177 GCCTA 180		
Db	867 ACTA 870		
RESULT 11			
AZ99964			
ID	AZ99964 standard; DNA; 2271 BP.		

XX AA299964;
 AC XX
 XX 25-JUL-2000 (first entry)
 DT XX
 DE DNA encoding a human osteoprotegerin ligand (OPGL).
 XX
 KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 185..1138
 FT /*tag= a
 FT /product= "osteoprotegerin ligand"
 PN MO200015807-A1.
 PD 23-MAR-2000.
 XX
 PE 13-SEP-1999; 99WO-DK00481.
 XX
 PR 15-SEP-1998; 98DK-0001164.
 PR 02-OCT-1998; 98US-0102896.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Halkier T, Haaning J;
 DR WPI: 2000-271444/23.
 DR P-PSDB: AAY84417.
 XX
 PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 XX to treat, prevent and ameliorate osteoporosis -
 PS Disclosure; Page 75-77; 110pp; English.
 XX
 CC The present sequence encodes a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 CC
 XX Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;
 SO

Query Match 47.3%; Score 96.4; DB 21; Length 2271;
 Best Local Similarity 74.5%; Pred. No. 3.2e-23;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

OY 3 TGAGGCTCATTAAGAGAGCTTTCTTGGAAACATGACCAAGATTGGCAACGCTTC 62
 DB 715 TGGTTCCTCATTAAGAGAGCTTCTCTTGGTACCATGATCGGGTGGCAAGATCTC 774
 OY 63 CAACATGACTTTCACCAAGCAAGAACTAAGATCA-----AAGGATTTATTACCGGAA 116
 DB 775 CAACATGACTTTCACCAAGCAAGAACTAAGTATATCAGATGGCTTTATTACCTGTA 834
 OY 117 TGGCGACATTTGCTGCACATCGGTAACCTGACAGAGCTTAAGTCTGACGACCTTCA 176
 DB 835 TGGCAACATTTGCTTGCACATCATGAAGTTCAGAGAGCTAGCTACAGATATCTTCA 894

OY 177 GCTA 180
 DB 895 ACTA 898

RESULT 12
 ID AAV70285
 XX AAV70285 standard; DNA; 2274 BP.
 AC AAV70285;
 XX
 DT 11-FEB-1999 (first entry)
 DE Human osteoprotegerin binding protein from the pcDNA/huOPSP1.insert.
 XX
 DE Human osteoprotegerin binding protein; OPB binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODR;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 185..1138
 FT /*tag= a
 FT /product= "osteoprotegerin binding protein"
 PN MO9846751-A1.
 PD 22-OCT-1998.
 XX
 PE 15-APR-1998; 98WO-US07584.
 XX
 PR 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ;
 DR WPI: 1998-594578/50.
 DR P-PSDB: AAW83195.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 XX e.g. treating bone diseases by modulating osteoclast differentiation
 XX and for diagnosis
 PS Claim 1; Fig 4; 47pp; English.
 XX
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 SO Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
 Query Match 47.3%; Score 96.4; DB 19; Length 2274;

XX TNF like proteins for treating autoimmunity and cancer
 XX
 XX
 PS Claim 1; Fig 1; 164pp; English.
 XX

CC The present sequence encodes human TNF-related activation induced
 CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
 CC variants, fragments, derivatives or analogues may be used as modulators
 CC of immune response in a mammal comprising, antisense sequences to
 CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
 CC Agonists and antagonists of TRANCE, can be used to modulate immune
 CC response by increasing or decreasing the life span of mature dendritic
 CC cells and increasing or decreasing the life span of mature dendritic
 CC are especially useful for treating immune system related conditions such
 CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
 CC The TRANCE polypeptides can be used to increase the viability of
 CC dendritic cells in vivo or in vitro, especially when used in conjunction
 CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
 CC CD40L or TNF-alpha).

XX
 SQ Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

Query Match 45.7%; Score 93.2; DB 20; Length 1823;
 Best Local Similarity 73.4%; Pred. No. 3.9e-22;
 Matches 135; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

OY 3 TGAGGCTCAAAACGAGCTTCTCTTGGAAACATGACCAAGATTGGCAACGCTCTC 62
 Db 315 TGCTTCCCAATAAGTAGTCTCTCTTGGTACATGATGGGGGTAAAGATCTC 374
 OY 63 CAACATGACTTTCAGCAGGAAACTAAGAGTCA-----AAGCATTTATTACGGGAA 116
 Db 375 CAACATGACTTTCAGCAGGAAACTAAGAGTCA-----AAGCATTTATTACGGGAA 116
 OY 117 TGGCGCATTTGCTCGACATCGCGTAACCTCAGAGGCGTAACTCTGAGGACCTTCA 434
 Db 435 TGGCGCATTTGCTCGACATCGCGTAACCTCAGAGGCGTAACTCTGAGGACCTTCA 434
 OY 177 GCTA 180
 Db 495 ACTA 498

RESULT 15
 AAF86481

ID AAF86481 standard; CDNA; 957 BP.

AC AAF86481;

DT 29-JUN-2001 (first entry)

DE Rat osteoclast differentiation factor, ODF, coding sequence.

KW Rat; osteoclast formation inducer; vaccine; gene therapy;

KW Osteoclast Differentiation Factor; bone; ss.

OS Rattus sp.

XX
 XX
 FT Key Location/Qualifiers
 FT CDS 1..957
 FT /tag= a
 FT /product= "Rat ODF"

PN MO200123549-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-AU01202.

PR 29-SEP-1999; 99AU-0003147.

XX (UYWA-) UNIV WESTERN AUSTRALIA.
 XX

PI Xu J, Zheng M;
 DR WPI: 2001-335526/35.
 DR P-PSDB: AAB82092.
 XX

PT Novel nucleic acid encoding rat osteoclast differentiation factor
 PT useful for modulating activity of a cell, e.g., cell proliferation,
 PT cell differentiation and cell viability.
 XX
 PS Claim 1; Fig 1; 81pp; English.

CC The present sequence is the coding sequence for rat Osteoclast
 CC Differentiation Factor (ODF). ODF is thought to be directly involved in
 CC the differentiation of monocytes/macrophages into osteoclasts.
 CC Osteoclasts promote dissolution of the bone matrix and solubilisation of
 CC bone salts. The present sequence is useful in gene therapy, and as
 CC hybridisation probes or primers. ODF protein is useful for modulating the
 CC activity of cells, e.g., cell proliferation, cell differentiation and
 CC cell viability, as immunogens to generate anti-rat ODF antibodies, and
 CC as vaccines. Anti-rat ODF antibodies are useful in assay methods for
 CC quantifying ODF polypeptides.
 XX

SQ Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;

Query Match 41.2%; Score 84; DB 22; Length 957;
 Best Local Similarity 71.3%; Pred. No. 4.9e-19;
 Matches 127; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

OY 8 CTCATAAAGCAGCTCTCTTCTTGGAAACATGACCAAGATTGGCAACGCTCCACA 67
 Db 539 CCCATAAAGCAGCTCTCTCTTGGTACATGATCGAGCGTGGCCAAAGATCTTACA 598
 OY 68 TGACTTTCAGCAACGGAATAAGAGTCA-----AAGCATTTATTACCGGAATGCC 121
 Db 599 TGAGCTTAAGCAACGGAATAAGAGTCA-----AAGCATTTATTACCGGAATGCC 121
 OY 122 ACATTGCTCTGACATCGCGTAACTCAGAGGCGTAACTCTGAGGACCTTCAGCT 179
 Db 659 ACATTGCTCTGACATCGCGTAACTCAGAGGCGTAACTCTGAGGACCTTCAGCT 179

Search completed: December 8, 2002, 17:26:22
 Job time : 65.0886 secs

Tue Dec 10 10:51:35 2002

us-09-880-457-1_copy_543_746.rge

Page 1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 16:41:40 : Search time 436.856 Seconds
(without alignments)
13590.225 Million cell updates/sec

Title: us-09-880-457-1_COPY_543_746
Sequence: 1 catgagcctataaacgag.....gtaattgagatcattcac 204

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmb1:*
1: gb_ha:*
2: gb_hcg:*
3: gb_lo:*
4: gb_lo:*
5: gb_lo:*
6: gb_lo:*
7: gb_lo:*
8: gb_lo:*
9: gb_lo:*
10: gb_lo:*
11: gb_lo:*
12: gb_lo:*
13: gb_lo:*
14: gb_lo:*
15: gb_lo:*
16: gb_lo:*
17: gb_lo:*
18: gb_lo:*
19: gb_lo:*
20: gb_lo:*
21: gb_lo:*
22: gb_lo:*
23: gb_lo:*
24: gb_lo:*
25: gb_lo:*
26: gb_lo:*
27: gb_lo:*
28: gb_lo:*
29: gb_lo:*
30: gb_lo:*
31: gb_lo:*
32: gb_lo:*
33: gb_lo:*
34: gb_lo:*
35: gb_lo:*
36: gb_lo:*
37: gb_lo:*
38: gb_lo:*
39: gb_lo:*
40: gb_lo:*
41: gb_lo:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	194	95.1	1186	6	AX358828
2	194	95.1	1186	6	AX362321
3	194	95.1	165707	2	AC104794
4	194	95.1	190748	9	AC010969
5	96.4	47.3	818	9	AB064268
6	96.4	47.3	911	9	AB061227
7	96.4	47.3	930	9	AB037599
8	96.4	47.3	954	6	AR156434
9	96.4	47.3	954	6	AR164148
10	96.4	47.3	972	9	AB064270
11	96.4	47.3	972	9	AB064269
12	96.4	47.3	1034	9	AF019047
13	96.4	47.3	2201	9	AF053712
14	96.4	47.3	2390	6	AX201362
15	96.4	47.3	2390	6	AX201362
16	96.2	47.2	113451	9	AF0323297
17	96.2	47.2	200724	9	AF139382
18	93.2	45.7	1823	9	AF013171
19	93.2	45.7	1823	9	AF013171
20	84	41.2	957	10	AF187319
21	84	41.2	127812	2	AC094149
22	80.8	39.6	754	10	AB032772
23	80.8	39.6	864	10	AB032771
24	80.8	39.6	951	6	E34350
25	80.8	39.6	951	6	E36388
26	80.8	39.6	951	10	AB036798
27	80.8	39.6	951	10	AB036798
28	80.8	39.6	1630	6	AR156433
29	80.8	39.6	1630	6	AR164147
30	80.8	39.6	1630	6	AR164147
31	80.8	39.6	1694	6	AX451897
32	80.8	39.6	2029	6	E34349
33	80.8	39.6	2029	10	AB022036S4
34	80.8	39.6	2191	6	AR157058
35	80.8	39.6	2191	6	AX140162
36	80.8	39.6	2225	10	AF019048
37	80.8	39.6	2237	10	AF013170
38	80.8	39.6	2295	6	AR062119
39	80.8	39.6	276831	2	AC126690
40	80.8	39.6	276831	2	AX232589
41	79.2	35.4	17.4	9	AC010719
42	35.4	17.4	140545	9	AL606844
43	35	17.2	175695	2	AL512635
44	35	17.2	176631	9	AL512635
45	33.8	16.6	151734	2	AC021225

ALIGNMENTS

RESULT 1	AX358828	1186 bp	DNA	linear	PAT 13-FEB-2002
LOCUS	AX358828				
DEFINITION	Sequence 81 from Patent WO0193983.				
ACCESSION	AX358828				
VERSION	AX358828.1	GI:18675315			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,				
AUTHORS	Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,				
	Watanabe, C.K., and Wood, W.I.				

Pred. No. is the number of results predicted by chance to have a

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0193983-A 81 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES Location/Qualifiers
 source 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 95.1%; Score 194; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 3.8e-53;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGAGGCTCATAAACAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 DB 504 CATGAGGCTCATAAACAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 OY 61 TCCACATGACTTTCAGCAACGGAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 DB 564 TCCACATGACTTTCAGCAACGGAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 OY 121 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTTCAGACCTTCAGCTA 180
 DB 624 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTTCAGACCTTCAGCTA 180
 OY 181 TGGTGTATTATTGAG 194
 DB 684 TGGTGTATTATTGAG 697

RESULT 2 AX362321 1186 bp DNA linear PAT 15-FEB-2002
 LOCUS AX362321
 DEFINITION Sequence 81 from Patent WO0208288.
 ACCESSION AX362321
 VERSION AX362321.1 GI:18694618
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K., and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 81 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN
 Query Match 95.1%; Score 194; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 3.8e-53;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGAGGCTCATAAACAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 DB 504 CATGAGGCTCATAAACAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 OY 61 TCCACATGACTTTCAGCAACGGAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 DB 564 TCCACATGACTTTCAGCAACGGAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 OY 121 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTTCAGACCTTCAGCTA 180
 DB 624 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTTCAGACCTTCAGCTA 180

OY 181 TGGTGTATTATTGAG 194
 DB 684 TGGTGTATTATTGAG 697

RESULT 3 AC104794 165707 bp DNA linear HTG 30-APR-2002
 LOCUS AC104794
 DEFINITION Homo sapiens chromosome 2 clone RP11-254F7, WORKING DRAFT SEQUENCE.
 ACCESSION AC104794
 VERSION 3 unrounded pieces.
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 3 (bases 1 to 165707)
 Waterston, R.H.
 Direct Submission
 Submitted (30-APR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Apr 30, 2002 this sequence version replaced g1:19339129.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 Project Information
 Center project name: H_NH0254F07

----- Summary Statistics -----
 Sequencing vector: M13, 0%
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Assembly program: Phrap, version 0.990319
 Consensus quality: 162662 bases at least Q40
 Consensus quality: 163189 bases at least Q30
 Insert size: 9479; agarose-fp
 Insert size: 167795; sum-of-contigs
 Quality coverage: 12.78 in Q20 bases; agarose-fp
 Quality coverage: 10.53 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1112: contig of 1112 bp in length
 * 1113 1212: gap of unknown length
 * 1213 76227: contig of 75015 bp in length
 * 76228 76327: gap of unknown length
 * 76328 165707: contig of 89380 bp in length.
 FEATURES
 source Location/Qualifiers
 1..165707

```

misc_feature      /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /chromosome="2"
                  /clone="RP11-254F7"
                  1.1112
misc_feature      /note="assembly_name:Contig21"
                  1213.76227
misc_feature      /note="assembly_name:Contig68"
                  76328.165707
misc_feature      /note="assembly_name:Contig69"
                  42242 c 39083 g 41295 t 200 others
BASE COUNT      42887 a 42242 c 39083 g 41295 t 200 others
ORIGIN
Query Match      95.1%; Score 194; DB 2; Length 165707;
Best Local Similarity 100.0%; Pred. No. 4.2e-53;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGAGCTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGCAACGCTC 60
    |||
DB 41177 CATGAGCTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGCAACGCTC 41236
    |||
QY 61 TCCACATGACTTTCAGCAACGAAACTAGAGTCAAGGATTTATTACCGGATGCC 120
    |||
DB 41237 TCCACATGACTTTCAGCAACGAAACTAGAGTCAAGGATTTATTACCGGATGCC 41296
    |||
QY 121 GACATTTGCTCTGCACATGCGCTAACCTAGAGGCTTAACCTGAGACCTTCAGCTA 180
    |||
DB 41297 GACATTTGCTCTGCACATGCGCTAACCTAGAGGCTTAACCTGAGACCTTCAGCTA 41356
    |||
QY 181 TGGTGAATTTGAG 194
    |||
DB 41357 TGGTGAATTTGAG 41370
    |||

RESULT 4
AC010969/c      AC010969      190748 bp      DNA      linear      PRI 07-NOV-2001
LOCUS
DEFINITION      Homo sapiens BAC clone RP11-95D17 from 2, complete sequence.
ACCESSION      AC010969
VERSION      AC010969.11 GI:13677120
KEYWORDS
SOURCE
ORGANISM      Homo sapiens.
                Homo sapiens. Chordata; Craniata; Vertebrata; Euteleostomi;
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                1 (bases 1 to 190748)
                Toward a complete human genome sequence
                Sulston, J.E. and Waterston, R.
                Genome Res. 8 (11), 1097-1108 (1998)
                99063792
MEDLINE
PUBMED      9847074
                2 (bases 1 to 190748)
                Sun, H., Abbott, A. and Le, T.P.
                The sequence of Homo sapiens BAC clone RP11-95D17
                Unpublished
                3 (bases 1 to 190748)
                Waterston, R.H.
                Direct Submission
                Submitted (28-SEP-1999) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
                4 (bases 1 to 190748)
                Waterston, R.H.
                Direct Submission
                Submitted (19-APR-2001) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
                5 (bases 1 to 190748)
                Waterston, R.H.
                Direct Submission
                Submitted (20-APR-2001) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA

```

REFERENCE

6 (bases 1 to 190748)
 Waterston, R.
 Direct Submission
 Submitted (07-NOV-2001) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Apr 19, 2001 this sequence version replaced gi:11128441.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.edu
 ----- Summary Statistics
 Center project name: H.NH0095D17

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., paired quality >
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
 donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
 Tatenno, M., Catanesi, J.J. and de Jong, P.J. (1996) An improved
 approach for construction of bacterial artificial chromosome
 libraries. *Genomics* 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
 and coworkers at the Roswell Park Cancer Institute
 (<http://drcpac.med.buffalo.edu>)

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-52D12. Actual start of
 this clone is at base position 1 of RP11-95D17; actual end is at
 base position 190748 of RP11-95D17.

There are polymorphic base differences between RP11-95D17 and the
 redundant clone AC062035. Data from AC062035 was used to finish
 RP11-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Size
 information from restriction digest suggests that the full repeat
 may not be represented.

FEATURES

source

Location/Qualifiers
 1..190748
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-95D17"
 /clone_id="RP11-11"
 185..230
 /rpt_family="L2"
 325..805
 /rpt_family="L1"
 806..1114
 /rpt_family="Alu"
 1449..1567
 /rpt_family="MIR"
 2179..2369
 repeat_region
 repeat_region
 repeat_region
 repeat_region

repeat_region	/rpt_family="MIR"	2626. .3646
repeat_region	/rpt_family="L2"	3716. .3745
repeat_region	/rpt_family="AT-rich"	3798. .4101
repeat_region	/rpt_family="Alu"	4196. .5255
repeat_region	/rpt_family="L1"	5256. .5559
repeat_region	/rpt_family="Alu"	5560. .6453
repeat_region	/rpt_family="L1"	6939. .6969
repeat_region	/rpt_family="MIR"	7701. .8007
repeat_region	/rpt_family="Alu"	8242. .8532
repeat_region	/rpt_family="MERL_type"	8533. .8834
repeat_region	/rpt_family="Alu"	8835. .9300
repeat_region	/rpt_family="MERL_type"	9322. .9647
repeat_region	/rpt_family="L2"	9632. .9784
repeat_region	/rpt_family="MIR"	9784. .9848
repeat_region	/rpt_family="Alu"	9862. .10061
repeat_region	/rpt_family="L1"	10062. .10360
repeat_region	/rpt_family="Alu"	10361. .10646
repeat_region	/rpt_family="L1"	10647. .10948
repeat_region	/rpt_family="Alu"	10949. .11090
repeat_region	/rpt_family="L1"	11135. .11420
repeat_region	/rpt_family="Alu"	11424. .11704
repeat_region	/rpt_family="L1"	11705. .12015
repeat_region	/rpt_family="Alu"	12016. .12045
repeat_region	/rpt_family="L1"	12047. .12327
repeat_region	/rpt_family="Alu"	12335. .12416
repeat_region	/rpt_family="L1"	12467. .12594
repeat_region	/rpt_family="Alu"	12596. .12678
repeat_region	/rpt_family="L1"	12698. .12954
repeat_region	/rpt_family="Alu"	12955. .13085
repeat_region	/rpt_family="Alu"	13194. .13433
repeat_region	/rpt_family="L2"	13557. .13667
misc_feature	/rpt_family="Alu"	13614. .14110
misc_feature	/note="similar to	13623. .14122
misc_feature	/note="similar to	13630. .14128
misc_feature	/note="similar to	13635. .14128
misc_feature	/note="similar to	13688. .13942
misc_feature	/note="similar to	EST BF770793 (NID:g12118693)"

misc_feature	13727. .14127	/note="similar to EST BF770796 (NID:g12118696)"
misc_feature	13729. .14126	/note="similar to EST BF770791 (NID:g12118691)"
repeat_region	13735. .13801	/rf_family="MIR"
misc_feature	14062. .14259	/note="similar to EST AL545813 (NID:g12878338)"
misc_feature	14144. .14259	/note="similar to EST BF659834 (NID:g11985242)"
misc_feature	14203. .14259	/note="similar to EST BF668191 (NID:g11942086)"
misc_feature	14229. .14259	/note="similar to EST AL571368 (NID:g12938594)"
misc_feature	14422. .14474	/note="similar to EST BE888644 (NID:g10345155)"
repeat_region	14851. .15156	

Query Match	95.1%	Score 194:	DB 9:	Length 150748:
Best Local Similarity	100.0%:	Pred. No. 4.2e-53:		
Matches 194:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY 1	CATGAGGCTCATTAACGAGCTTTTCTTTGGAAACATGACCAGATGGGCAACGTC			
Db 174428	CATGAGGCTCATTAACGAGCTCTTCTCTTGGAAACATGACCAGATTTGGCAACGTC			
QY 61	TCCACATGACTTTTGGCAACGGAAACCTAAGAGTCGAAGGCTATTATTACCGGAATGCC			
Db 174368	TCCACATGACTTTTGGCAACGGAAACCTAAGTCGAAGGCTATTATTACCGGAATGCC			
QY 121	GACATTTCGTCGCACTGCGCTAACCTGCACAGGCGCTAACCTGCGACGACCTTCACGTA			
Db 174308	GACATTTCGTCGCACTGCGCTAACCTGCACAGGCGCTAACCTGCGACGACCTTCACGTA			
QY 181	TGCGTAAATTGAG 194			
Db 174248	TGCGTAAATTGAG 174235			

RESULT 5	AB064268	AB064268	818 bp	mRNA	linear	PRI 26-DEC-2001
LOCUS	AB064268					
DEFINITION	Homo sapiens hRANKL 3					
ACCSSION	AB064268					
VERSION	AB064268.1					
KEYWORDS	GI:18143616					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
	cdna to mRNA.					

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
Ikeda, T., Kuroyama, H. and Hirokawa, K.
Determination of human RANKL isoforms
2 (bases 1 to 818)
Ikeda, T. and Kuroyama, H.
Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda Tohru Ikeda

FEATURES	Location/Qualifiers
source	1. .818

```
gene      /organism="Homo sapiens"  
          /db_xref="taxon:9606"  
          1..818  
          /gene="hRANKL 3"  
          84..818  
          /gene="hRANKL 3"  
          /codon_start=1  
          /product="receptor activator of nuclear factor kappa B
```


ORIGIN	Score	DB	length
Query Match	47.38;	96.4;	911;
Best local Similarity	74.58;	Pred. No. 8.7e-21;	

Query Match	74.3%	Score 96.4	DB 9	Length 930
Similarity	47.5%	Pred. No. 8.7e-21		
Best Local				
Matches 137	Conservative	0	Mismatches 41	Indels 6
				Gaps

QY 3 TGAGGCTCATAAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 406 TGGTCCCATTAAGTAGAGCTCTCTCTGTGACATGATCGGGTTGGGCCAAGATCTC 465
 QY 63 CAACATGACTTTGACGACGAAAGAACTAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 466 CAACATGACTTTTACCAATGGAATACTAATAGTATATCATGATGGCTTTATTACCTGTA 525
 QY 117 TGGCGACATTTGCTCTGACATCGGCTAACCTCAGACGCTTAAGTCTGACGAGCTTCA 176
 Db 526 TGGCAACATTTGCTTTCACATCATGAAACTTCAGAGACCTAGCTACAGATATCTTCA 585
 QY 177 GCTA 180
 Db 586 ACTA 589

RESULT 8
 ARI56434
 LOCUS ARI56434 954 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 12 from patent US 6242213.
 ACCESSION ARI56434
 VERSION ARI56434.1 GI:15125138
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 954)
 AUTHORS Anderson,D.M.
 TITLE Isolated DNA molecules encoding RANK-L
 JOURNAL Patent: US 6242213-A 12 05-JUN-2001;
 FEATURES
 source 1..954
 /organism="unknown"

BASE COUNT 255 a 239 c 227 g 233 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 6; Length 954;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 531 TGGTCCCATTAAGTAGAGCTCTCTGTGACATGATCGGGTTGGGCCAAGATCTC 465
 QY 63 CAACATGACTTTGACGACGAAAGAACTAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 591 CAACATGACTTTTACCAATGGAATACTAATAGTATATCATGATGGCTTTATTACCTGTA 525
 QY 117 TGGCGACATTTGCTCTGACATCGGCTAACCTCAGACGCTTAAGTCTGACGAGCTTCA 176
 Db 651 TGGCAACATTTGCTTTCACATCATGAAACTTCAGAGACCTAGCTACAGATATCTTCA 585
 QY 177 GCTA 180
 Db 711 ACTA 714

RESULT 9
 ARI64148
 LOCUS ARI64148 954 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 12 from patent US 6271349.
 ACCESSION ARI64148
 VERSION ARI64148.1 GI:16235114
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 954)
 AUTHORS Douglall,W.C. and Galibert,L.
 TITLE Receptor activator of NF- κ B
 JOURNAL Patent: US 6271349-A 12 07-AUG-2001;
 FEATURES Location/Qualifiers

source 1..954
 /organism="unknown"
 BASE COUNT 255 a 239 c 227 g 233 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 6; Length 954;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 531 TGGTCCCATTAAGTAGAGCTCTCTGTGACATGATCGGGTTGGGCCAAGATCTC 465
 QY 63 CAACATGACTTTGACGACGAAAGAACTAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 591 CAACATGACTTTTACCAATGGAATACTAATAGTATATCATGATGGCTTTATTACCTGTA 525
 QY 117 TGGCGACATTTGCTCTGACATCGGCTAACCTCAGACGCTTAAGTCTGACGAGCTTCA 176
 Db 651 TGGCAACATTTGCTTTCACATCATGAAACTTCAGAGACCTAGCTACAGATATCTTCA 710
 QY 177 GCTA 180
 Db 711 ACTA 714

RESULT 10
 AX147989
 LOCUS AX147989 954 bp DNA linear PAT 08-JUN-2001
 DEFINITION Sequence 12 from Patent WO0136637.
 ACCESSION AX147989
 VERSION AX147989.1 GI:14346964
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 954)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE Receptor activator of nf- κ B
 JOURNAL Patent: WO 0136637-A 12 25-MAY-2001;
 FEATURES
 source 1..954
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..954
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CA41185.1"
 /db_xref="GI:14346965"
 /translation="MRRASRDYTKYLRGSEMGGPGAPHEPLAPPPAPPPAPPA
 SRMEVALLGLIGOVVCSVALFFFPRAQDPBRISDPDHCYRILRLHENDFQDT
 TLESODTKLIPDSGRIRKQAFQAGVOKELOHIVGSHIRAKMADVGSWDLAKRSKL
 EAQPFALHTINATIDIPSGSHKYSLSWYHDGRGAKISNPKYSKGLIVQDGFYLYLA
 NICEFHETSGDIATEYLIQMYVTYSIKLPSHLMGSGYKYSWNSSEHFYSIN
 VGSFEKLRGSEIETSVNSLDDPDQDNYFQAFKVRDID"

BASE COUNT 255 a 239 c 227 g 233 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 6; Length 954;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 531 TGGTCCCATTAAGTAGAGCTCTCTGTGACATGATCGGGTTGGGCCAAGATCTC 465
 QY 63 CAACATGACTTTGACGACGAAAGAACTAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 591 CAACATGACTTTTACCAATGGAATACTAATAGTATATCATGATGGCTTTATTACCTGTA 525
 QY 117 TGGCGACATTTGCTCTGACATCGGCTAACCTCAGACGCTTAAGTCTGACGAGCTTCA 176

	Db	651	TGCCAACATTTGCTTTCGCACATCATCAAGAACTTGACGAGACCTACTACAGATATTCTTCA	710
OY	177	GCTA	180	
Db	711	ACTA	714	
RESULT 11				
AX451895				
LOCUS				
DEFINITION	AX451895	954 bp	DNA	linear
ACCESSION	Sequence 5 from Patent WO0224896.			PAT 03-JUL-2002
VERSION	AX451895			
KEYWORDS	AX451895.1 GI:21698735			
SOURCE	.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
JOURNAL	Dougal J.W.C.			
FEATURES	Screening assays for agonists or antagonists of receptor activat or of nf-kb Patent: WO 0224896-A 5 28-MAR-2002; IMMUNEX CORPORATION (US) Location/Qualifiers 1..954 /organism="Homo sapiens" /db_xref="taxon:9606" 1..954 /note="unnamed protein product" /codon_start=1 /protein_id="CAD37794.1" /db_xref="gi:21698736" /translation="MRASRDYTKRYLSPSEMGSGPGAPHEGLNAPPAPHOPEAA /translaltion="MRASRDYTKRYLSPSEMGSGPGAPHEGLNAPPAPHOPEAA SRSMVALGLGLQVYCVALPFPFAOMDPRISEDGHICYLRLRHNADRODT TLESODTLIPDSCKRIKOAFOGAOKDELQIHIVGSOHIRAEKAMVDGSLDLAKSKL EAOPFAHLITNADIPSGSHKVSLSMTFHDGRNAKISNMFTSGKLIVNDPEYLYA NICFHHTSGDLATEYLIQLWLVYTSTIKIIPSSHILMKGGSTRKYMSGEHFYSIN VGCFKRSGEIEISLEVENSPFLDDPDADYTFGAFAFKVIDID"			
CDS				
BASE COUNT	255 a	239 c	227 g	233 t
ORIGIN				
	Query Match	47.3%;	Score 96.4;	DB 6; Length 954;
	Best Local Similarity	74.5%;	Pred. No. 8.7e-21;	
	Matches 137; Conservative	0;	Mismatches 41;	Indels 6; Gaps 1;
OY	3	TGAGCGCATAAAAACGAGCTTCTCTCTTGGAACATGCACCAAGATTGGCCAAACGTCTC	62	
Db	531	TGTTTTCCCAATTAAGTAGTGCTGTCTGCTTGATGCATGATCGGGGTGGCCAAAGATCTC	590	
OY	63	CAACATGACTTTCAGCACAGGAAACTAGAGTCA-----AAGCATTTATTACC GGAA	116	
Db	591	CAACATGACTTTCAGCAATGAGAAACTAAATAATGTAATCAGAGATGGCTTTTATTACTGTGA	650	
OY	117	TGCCGACATTTGCTCTGAGCATGCGCTGAACCTAGCAGAGGCTTAACCTCAGAGACCTTCA	176	
Db	651	TGCCAACAATTGCTTTGCACATCATGAANAATTTCAGGAGACCTAGCTACAGAGATCTTCA	710	
OY	177	GCTA	180	
Db	711	ACTA	714	
RESULT 12				
AB064270				
LOCUS				
DEFINITION	AB064270	972 bp	mRNA	linear
ACCESSION	Homo sapiens hRAKL 2-2 mRNA for receptor activator of nuclear			PRI 26-DEC-2001
VERSION	AB064270			
KEYWORDS	AB064270.1 GI:18143620			
SOURCE	Homo sapiens CDNA to mRNA.			

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	Ikeda,T., Kuroyama,H. and Hirokawa,K. Determination of human RANKL isoforms unpublished
AUTHORS	Ikeda,T. and Kuroyama,H.
JOURNAL	2 (bases 1 to 972)
REFERENCE	Submitted Submission Direct Submissions Submitted (25-JUN-2001) Tohtu Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:tohtu.phd2med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
TITLE	Location/Qualifiers
AUTHORS	1. .972
JOURNAL	/organism="Homo sapiens"
REFERENCE	/db.xref="taxon:9606"
AUTHORS	1. .972
JOURNAL	/gene="hRANKL 2-2"
REFERENCE	160. 972
AUTHORS	/gene="hRANKL 2-2"
JOURNAL	/codon_start=1
REFERENCE	/product="receptor activator of nuclear factor kappa B
AUTHORS	ligand 2-2"
JOURNAL	/protein_id="BAB79695.1"
REFERENCE	/db_xref="gi:18143621"
AUTHORS	/translation="MFVALDLGLGIGVYCSVALFFFRQMDPNRISEGGTCTIRIL
JOURNAL	RLLNADFDODTTLESODTKLIPDSCKRIKAFQGAAYOKELQHVGSOHRBAKNWDG
REFERENCE	SWLDLARKSKLEAPFALFTLNATIDLPSCSHKSLSSWHDRLGMATISMTSNGKL
AUTHORS	VNOGDFLYLVNLCFRHHETSGDATLDMVYRTSIKIKPSHTLKGGSTIWS
JOURNAL	GNSHFYSINVGFEFKLRSESEISIVSNPSSLDPDDPATYFGARVDID"
BASE COUNT	270 a 219 c 249 g 234 t
ORIGIN	
Query Match	47.3%; Score 96.4; DB 9; Length 972;
Best Local Similarity	74.5%; Pred. No. 8.7e-21;
Matches 137; Conservative	0; Mismatches 41; Indels 6; Gaps 1;
Db	3 TGAGCGTCATAAACAAGCTTCTTGGAACATGCACAAGATTGGCAACGCTC 62
OY	
Db	549 TGGTCCCATAAAGTAGTGCTGTCTTGTCGNACATGATCGGGTTGGCCACAAGATCTC 608
OY	63 CAATGACTTTTCGCAACGGAAGAAGTAAGATCA-----AAGCATTTATTACGGAA 116
Db	609 CAATGACTTTTATGCAATGGAAGAACTAATAGTTATTCAGAGATGCGTTATTACCTGTA 668
OY	117 TGCCGACATTTGCTCTGCAGATCGCGTAACCTCAGCAGCGCTACACTTCGACGACCTTCA 176
Db	669 TGCCAACATTTGCTTGCAGATCTGAAACTTACGAGAGACCTACAGAGATCTTCA 728
OY	177 GCTA 180
Db	729 ACTA 732
RESULT 13	
AB064269	AB064269 1034 bp mRNA linear pri 26-DEC-2001
LOCUS	Homo sapiens hRANKL 1 mRNA for receptor activator of nuclear factor
DEFINITION	kappa B ligand 1, complete cds.
ACCESSION	AB064269
VERSION	AB064269.1 GI:18143618
KEYWORDS	.
SOURCE	Homo sapiens cDNA to mRNA.
ORGANISM	Homo sapiens
EUKARYOTA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MAMMALIA	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	Ikeda,T., Kuroyama,H. and Hirokawa,K. Determination of human RANKL isoforms unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1034)
Ikeda, T. and Kuroyama, H.
Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Immunology, Graduate
School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail: tohru.ph2med.tmd.ac.jp, Tel: 81-3-5803-5176,
Fax: 81-3-5803-0123)

FEATURES

Location/Qualifiers
1..1034

/organism="Homo sapiens"

/db_xref="taxon:9606"

gene

CDS

81..1034

/gene="hRANKL 1"

/codon_start=1

/product="receptor activator of nuclear factor kappa B

ligand 1"

/protein_id="BAB9694.1"

/db_xref="GI:18143619"

/translation="MRASRDYTKYLRGSENGGCGAPHEGFLHAPPPAPHPAPPA

TLESODTKLIPSCRIKQAFQAVQKELQHTVSGHIAEKAMVDGSLDLAKRSKL

EAQPFRLHNTNIDIPSGSHKVSLSWYHDROMAKISNMTFSNGKLIYVODGFYLYA

NICFRHETSGDLATEYQLMIVYVTKTSIKIPSSHTLMKGSTKYSNGSSEHFYSIN

VGFRFLRSGEISIEVSNPSLDDPDATYFGAFKVRID"

BASE COUNT

275 a

257 c

265 g

237 t

Query Match

Best Local Similarity 74.5%; Score 96.4; DB 9; Length 1034;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTATAAAGACGCTCTTCTTCTTGAACATGACCAAGATTGGCGCAAGCTTC 62

DB 611 TGGTTCCTATAAAGACGCTCTTCTTGTGACATGATGCGGGGTGGCCCAAGATCTC 670

QY 63 CAACATGACTTTCACGACGAAAGCTAAGCTCA-----AAGCATTTATTACCGGAA 116

DB 671 CAACATGACTTTCACGACGAAAGCTAAGCTCA-----AAGCATTTATTACCGGAA 116

QY 117 TGGCGACATTTGCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTCGCAGGACCTTCA 176

DB 731 TGGCAACATTTGCTTTCGACATCATGAACCTTCAGAGACCTAGCTACAGATATCTTCA 790

QY 177 GCTA 180

DB 791 ACTA 794

RESULT 14

AF019047

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homosapiens

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

Anderson, D.M., Billingsley, W., Dougal, W., Maraskovsky, E.,

Galibert, L.,

Tometsko, M.E., Roux, E.R., Teepe, M.C., Dubose, R.F., Cosman, D., and

A homologue of the TNF receptor and its ligand enhance T-cell

growth and dendritic-cell function

Nature 390 (6556), 173-179 (1997)

JOURNAL

MEDLINE

PUBMED

9367155

2 (bases 1 to 2201)

AUTHORS

Anderson, D.M., Billingsley, W., Dougal, W., Maraskovsky, E.,

Cosman, D., Dubose, R. and Galibert, L.

Direct Submission

Submitted (13-AUG-1997)

Molecular Biology, Immunex Corp., 51

University St., Seattle, WA 98101, USA

Location/Qualifiers

1..2201

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="13"

/map="13q14"

gene

129..1082

/gene="RANKL"

/note="receptor activator of nuclear factor kappa B

ligand"

/product="RANKL"

/protein_id="AAB8681.1"

/db_xref="GI:2612922"

/translation="MRASRDYTKYLRGSENGGCGAPHEGFLHAPPPAPHPAPPA

TLESODTKLIPSCRIKQAFQAVQKELQHTVSGHIAEKAMVDGSLDLAKRSKL

EAQPFRLHNTNIDIPSGSHKVSLSWYHDROMAKISNMTFSNGKLIYVODGFYLYA

NICFRHETSGDLATEYQLMIVYVTKTSIKIPSSHTLMKGSTKYSNGSSEHFYSIN

VGFRFLRSGEISIEVSNPSLDDPDATYFGAFKVRID"

BASE COUNT

658 a

429 c

497 g

617 t

Query Match

Best Local Similarity 74.5%; Score 96.4; DB 9; Length 2201;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTATAAAGACGCTCTTCTTCTTGAACATGACCAAGATTGGCGCAAGCTTC 62

DB 659 TGGTTCCTATAAAGACGCTCTTCTTGTGACATGATGCGGGGTGGCCCAAGATCTC 718

QY 63 CAACATGACTTTCACGACGAAAGCTAAGCTCA-----AAGCATTTATTACCGGAA 116

DB 719 CAACATGACTTTCACGACGAAAGCTAAGCTCA-----AAGCATTTATTACCGGAA 116

QY 117 TGGCGACATTTGCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTCGCAGGACCTTCA 176

DB 779 TGGCAACATTTGCTTTCGACATCATGAACCTTCAGAGACCTAGCTACAGATATCTTCA 838

QY 177 GCTA 180

DB 839 ACTA 842

RESULT 15

AF053712

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homosapiens

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

Lacey, D.L., Timms, E., Tan, H.-T., Kelley, M.J., Dunstan, C.R.,

Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,

Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,

DeLaney, J., and Boyle, W.J.

Osteoprotegerin ligand is a cytokine that regulates osteoclast

differentiation and activation

Cell 93 (2), 165-176 (1998)

JOURNAL

MEDLINE

PUBMED

9568710

REFERENCE 2 (bases 1 to 2271)

AUTHORS Boyle,W.J.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
 One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES Location/Qualifiers

source
 1..2271
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 185..1138
 /function="regulates osteoclast differentiation and
 activation"
 /codon_start=1
 /product="osteoprotegerin ligand"
 /protein_id="AAC39731.1"
 /db_xref="GI:3057146"

CDS

/translation="MRRASRDYTKYLRSSEMGSGPAPHEGFLHAPPPAPHPAPPA
 SRMEVALGLGLGVCSVALFFYPRAQMDPNRISDGTGHCYRIILRLHENDAFDPT
 TLESODTKLIPDSCKRIKQAFQGVQKELQIYSGHIRAEKAMVDSWLDLAKRSKL
 EADPFAHLTINADIPSGSHKYSLSMYHNRGMAKISNMTFSGKLIYNQDGFYLYA
 NICEFRHETSGDIALEYLQLMVIVTKTSIKIPSSHTLMKGGSTKRWSGNSEFHFYSIN
 VGGFFRLRSGEISIEVSNPSLDPDQDAFYGAFAKVRDID"

BASE COUNT 658 a 462 c 522 g 629 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 9; Length 2271;
 Best Local Similarity 74.5%; Pred. No. 8.8e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

OY 3 TGAGCGTCATATAACAGAGTCTTCTCTGGAACATGACCAGATTGGCCAAACGTCTC 62
 || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 715 TGTTCCTCCATAAGTAGTCTGCTCTGTGTACCATGATCGGGGTGGCCAAAGATCTC 774
 OY 63 CAACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGGCATTATTACCGGAA 116
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 775 CAACATGACTTTCAGCAACGGAAGAACTAAGAGTCAAGATGCGCTTTATTACCTGTA 834
 OY 117 TGGCGACATTTGCTCTGCAATCGGCTAACCTCAGCAGGCGCTTAACCTGCAGACCTTCA 176
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 835 TGCCACACTTTGGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCA 894
 OY 177 GCTA 180
 ||||
 Db 895 ACTA 898

Search completed: December 8, 2002, 18:33:58
 Job time : 553.856 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:16:58 ; Search time 576.736 Seconds
(Without alignments)
7329.213 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atggcaatcctgacgctcag.....gtaattgagatcattcac 261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_hlc:*
12: gb_estcl3:*
13: gb_estcl4:*
14: gb_estcl5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95.8	36.7	659	AG107545	AG107545 Pan trogl
2	84.8	32.5	612	BH267783	BH267783 CH230-186
3	71	27.2	362	AV653073	AV653073 AV653073
4	38.6	14.8	198	BG197160	BG197160 RST16397
5	37	14.2	276	BG203357	BG203357 RST22738
6	37	14.2	277	BG184205	BG184205 RST3126 A

Result No.	Score	Query Match	Length	DB ID	Description
7	37	14.2	299	BG206497	BG206497 RST5946
8	35.8	13.7	697	AZ897813	AZ897813 RPT1-24-2
9	34.8	13.3	724	BH671765	BH671765 BOMKY36TR
10	34.2	13.1	463	BF930674	BF930674 MR2-MT013
11	34.2	13.1	536	BM892233	BM892233 sam57H07
12	34.2	13.1	596	BE661877	BE661877 6-C8 Gmax
13	34	13.0	475	BE346444	BE346444 SP25104.Y
14	34	13.0	563	AF046628	AF046628 AF046628
15	34	13.0	631	AG132233	AG132233 Pan trogl
16	34	13.0	735	BH794645	BH794645 ME_MBA000
17	34	13.0	1027	BQ050697	BQ050697 ACENCOUPT
18	33.8	13.0	284	AL768846	AL768846 Arabidops
19	33.8	13.0	321	BG212237	BG212237 RST31821
20	33.6	12.9	530	AA310614	AA310614 EST18161
21	33.2	12.7	853	BH314331	BH314331 CH230-99C
22	33.2	12.7	865	AZ550383	AZ550383 ENTER44TR
23	32.8	12.6	407	AW750032	AW750032 PM2-BT054
24	32.8	12.6	561	AV979271	AV979271 AV979271
25	32.6	12.5	426	BM434433	BM434433 1RT10F11
26	32.4	12.4	435	AQ462091	AQ462091 HS-5118-B
27	32.4	12.4	823	AZ724950	AZ724950 RPT1-24-6
28	32.2	12.3	771	AZ724950	AZ724950 RPT1-24-6
29	32	12.3	533	BE070217	BE070217 B15 Chick
30	32	12.3	661	BQ839707	BQ839707 B15 Chick
31	32	12.3	819	BH419036	BH419036 BOCVW75TR
32	32	12.3	912	BE683775	BE683775 BOCVW75TR
33	32	12.3	930	BH150843	BH150843 BOCVW75TR
34	31.8	12.2	428	AU226504	AU226504 BNT0138TR
35	31.8	12.2	640	BB589964	BB589964 AU226504
36	31.8	12.2	839	CNS02TGO	AL213155 Tetradon
37	31.8	12.2	841	BF030090	BF030090 601557176
38	31.8	12.2	915	AZ684294	AZ684294 ENTCU94TR
39	31.8	12.2	966	CNS03AZE	AL235859 Tetradon
40	31.6	12.1	426	AO523546	AO523546 HS-5207_A
41	31.6	12.1	426	BJ445420	BJ445420 BJ445420
42	31.6	12.1	552	BT441726	BH741726 g136g03.g
43	31.6	12.1	552	BH725020	BH725020 BOMBNI1TR
44	31.6	12.1	642	BH714383	BH714383 BOMI40TR
45	31.6	12.1	800	BH672114	BH672114 BOMOT38TR

ALIGNMENTS

RESULT 1
AG107545 659 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
LOCUS AG107545
ACCESSION AG107545
VERSION AG107545.1 GI:16728063
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes male lymphoblast DNA, clone: lib:PTB Chimpanzee Male
BAC library clone: PTB-112G09.F.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE
BAC end sequences of library PTB
JOURNAL
Unpublished
2 (bases 1 to 659)
AUTHORS
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
DIRECT SUBMISSION
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Saitama-shi, Tsukuba-shi, Ibaraki, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
Telex: 81-45-503-9111, URL: http://gsc.riken.go.jp/
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the K&D process and may have higher chance of
clone tracking errors.

PRIMERS
Sequencing: -21M13
LIBRARY
Vector : PK5145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. .659
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-112G09.F"
/sex="male"
/cell_type="lymphoblast"
/clone_id="PTB Chimpanzee Male BAC Library"
BASE COUNT 181 a 168 c 121 g 189 t
ORIGIN

Query Match 36.7% Score 95.8; DB 17; Length 659;
Best Local Similarity 71.1% Pred. No. 5.1e-21;
Matches 143; Conservative 0; Mismatches 52; Indels 6; Gaps 1;
QY 43 ATACCATCATATCCATGAGCTCATATAAAGAGCTCTTCTTCTTGGAAACATGACCA 102
DB 388 ATGCTCTCTCTCCACAGCTTCCATAGTACTCTCTCTTGGTACCATGATCGG 447
QY 103 GATTGGCAACGCTCCATCATGCTTTCAGCAAGCAAACTAAGATCA-----AA 156
DB 448 GGTGGGCAAGATCTCCACATGACTTTTACGCAATGAAAACATAATGATATCAGAT 507
QY 157 GGCATTTATACCGGAATGCGGACATTTGCTCTGACATGCGGTACCTCGACAGCCTA 216
DB 508 GCGTTTATATACCTGATGCAACATTTGCTTTCGACATCATGAACCTTCAGAGACCTA 567
QY 217 ACCTTCGACGACCTTCAGCTA 237
DB 568 GCTACAGATATCTTCACTA 588

RESULT 2
BH267783/c 612 bp DNA linear GSS 30-NOV-2001
LOCUS CH230-186C1.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
DEFINITION BH267783
ACCESSION BH267783.1 GI:17180093
VERSION GSS.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 612)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
A., Gebregregis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-186C1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Plietier de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering/information.htm). BAC end
plate: 186 row: C column: 1
Seq primer: T7

FEATURES
Class: BAC ends.
Location/Qualifiers
source 1. .612
/organism="Rattus norvegicus"
/strain="BN/SSNhd/KCw"
/db_xref="taxon:10116"
/clone="CH230-186C1"
/clone_id="CHORI-230 Segment 1"
/sex="Female"
/note="Vector: pPARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNhd/KCw) BAC library produced by
Plietier de Jong"
BASE COUNT 168 a 145 c 133 g 166 t
ORIGIN

Query Match 32.5% Score 84.8; DB 17; Length 612;
Best Local Similarity 69.5% Pred. No. 1.6e-17;
Matches 132; Conservative 0; Mismatches 52; Indels 6; Gaps 1;
QY 53 TATCCATGAGGCTCATATAAAGAGCTCTTCTTCTTGGAAACATGACCAAGTGGCAA 112
DB 603 TCTCTAGAGTCCCATAAAGTACGTCTGCTCTTGGTACCATGATGAGGCGCA 544
QY 113 AGCTCCACATGACTTTAGCAACGGAACCTAAGATCA-----AAGCATTTATT 166
DB 543 AGATCTCTACATGACTTTAAGCAACGAAACATAAGGTTAACCAAGATGCTTCTATT 484
QY 167 ACCGGAATGCCGACATTTGCTCTGACATGCGGTACCTGACAGGCGCTACTGACAG 226
DB 483 ACCTGACGCAACATTTGCTTTCAGCATCATGAACCTCAGGAGCGTACCTCGGACT 424
QY 227 ACCTTACGCT 236
DB 423 ATCTTACGCT 414

RESULT 3
AV653073 362 bp mRNA linear EST 15-JAN-2002
LOCUS AV653073
DEFINITION AV653073 GLC Homo sapiens cDNA clone G1CDB01.3', mRNA sequence.
ACCESSION AV653073
VERSION AV653073.1 GI:9874087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 362)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Ou,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="G1CDB01"
/clone_id="GLC"
/tissue_type="corresponding non cancerous liver tissue"

FEATURES
source


```

/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      102 a      80 c      78 g      100 t      2 others
ORIGIN
Query Match      27.2%; Score 71; DB 10; Length 362;
Best Local Similarity 75.4%; Pred. No. 5.6e-13;
Matches 101; Conservative 0; Mismatches 31; Indels 2; Gaps 1;

OY 4 GCAATCTGACGCTGACGCTTCTGTTGTTATTAATACCATCATATTCATGAG 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 228 GCAAGCTTGAAGCTGACGCTTTGCTCATCTCATATTATTAATGACGACATCCCATCTG 287
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 64 GCT--CATTAAGAGCTCTTCTTCTTGAACATGACCAAGATTGGGCAACGTCCTCA 121
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 288 GTTCCCATTAAGTGAAGTGTGCTCTGTGACATGATCGGTTGGCCAAATCTTCCA 347
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 122 ACATGACTTTCAGC 135
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 348 ACATGACTTTCAGC 361
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 4
Bg197160/c      198 bp      mRNA      linear      EST 21-APR-2001
LOCUS      Bg197160
DEFINITION      RST16397 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION      Bg197160
VERSION      Bg197160.1 GI:13718847
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 198)
AUTHORS      Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Colhen,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE      Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL      Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE      21227151
COMMENT      Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 148.
Location/Qualifiers
1. 198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT      55 a      56 c      41 g      46 t
ORIGIN
Query Match      14.8%; Score 38.6; DB 12; Length 198;
Best Local Similarity 77.0%; Pred. No. 0.036;
Matches 47; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 4 GCAATCTGACGCTGACGCTTCAACATCTTGTATTATACCATATATCCATGAG 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

Db 116 GCAAGCTTGAAGCTGACGCTTTGCTCATCTCATATTATTAATGACGACATCCATGAG 57
OY 64 G 64
Db 56 G 56

RESULT 5
Bg203357/c      276 bp      mRNA      linear      EST 21-APR-2001
LOCUS      Bg203357
DEFINITION      RST22738 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION      Bg203357
VERSION      Bg203357.1 GI:13725044
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 276)
AUTHORS      Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Colhen,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE      Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL      Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE      21227151
COMMENT      Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 276.
Location/Qualifiers
1. 276
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT      92 a      51 c      59 g      74 t
ORIGIN
Query Match      14.2%; Score 37; DB 12; Length 276;
Best Local Similarity 75.4%; Pred. No. 0.15;
Matches 46; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4 GCAATCTGACGCTGACGCTTCAACATCTTGTATTATACCATATATCCATGAG 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 67 GCAAGCTTGAAGCTGACGCTTTGCTCATCTCATATTATTAATGACGACATCCATGAG 8
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 64 G 64
Db 7 G 7

RESULT 6
Bg184205/c      277 bp      mRNA      linear      EST 21-APR-2001
LOCUS      Bg184205
DEFINITION      RST3126 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION      Bg184205
VERSION      Bg184205.1 GI:13705892
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 277)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,J., Daniels,J., and Ducar,M.
 TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com

FEATURES
 source Location/Qualifiers
 1..277
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 94 a 51 c 58 g 74 t
 ORIGIN

Query Match 14.2% Score 37; DB 12; Length 277;
 Best Local Similarity 75.4% Pred. No. 0.15;
 Matches 46; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 GCAATCCTGACGCTCAGCTTCACTGATCTGTTATTAATACCATATATCCATAG 63
 Db 68 GCAAGCTTGAGCTCAGCTTTGCTCATCTCATATTAATGCGACGACATCCATCTG 9
 QY 64 G 64
 Db 8 G 8

RESULT 7
 BG206497/c 299 bp mRNA linear EST 21-APR-2001
 LOCUS RST25946 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG206497
 ACCESSION BG206497.1 GI:13728184
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM

REFERENCE 1 (bases 1 to 299)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,J., Daniels,J., and Ducar,M.
 TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com

FEATURES
 source High quality sequence stop: 299.
 Location/Qualifiers
 1..299
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 98 a 56 c 65 g 80 t
 ORIGIN

Query Match 14.2% Score 37; DB 12; Length 299;
 Best Local Similarity 75.4% Pred. No. 0.16;
 Matches 46; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 GCAATCCTGACGCTCAGCTTCACTGATCTGTTATTAATACCATATATCCATAG 63
 Db 90 GCAAGCTTGAGCTCAGCTTTGCTCATCTCATATTAATGCGACGACATCCATCTG 31
 QY 64 G 64
 Db 30 G 30

RESULT 8
 A2897813 697 bp DNA linear GSS 05-MAR-2001
 LOCUS RPCI-24-210N16.TJ RPCI-24 Mus musculus genomic clone RPCI-24-210N16
 DEFINITION A2897813
 ACCESSION A2897813
 VERSION A2897813.1 GI:13216758
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM

REFERENCE 1 (bases 1 to 697)
 AUTHORS Zhao,S., Nieman,W., Malek,J., Shatsman,S., Akimov,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregiorgis,E., Russell,D., de Jong,P., and Fraser,C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-24
 JOURNAL Unpublished (1999)
 COMMENT Other-GSSs: RPCI-24-210N16.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

CLONES are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end plates: 210 row: N column: 16
 Seq primer: SP6
 Class: BAC ends.
 FEATURES
 source Location/Qualifiers
 1..697
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="RPCI-24-210N16"
 /clone_lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTRABAC1; Site_1: BamHI; Site_2: BamHI;

DEFINITION	Sam5b07.y1 Gm.c1069 glycine max cdna clone S04EAF CLONE ID: F9013.24 PROTEIN. ;
ACCESSION	FM897233

ACCESSION	BM892233
VERSION	BM892233.1
KEYWORDS	EST.
SOURCE	GI:19347353

ORGANISM

REFERENCE AUTHORS

TITLE
 JOURNAL
 COMMENT
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-553-4363 or contact: curenresgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence step: 421.

```

FEATURES
source      Location/Qualifiers
1. .536

```

```

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl069-3805"
/clone_1fb="Gm-cl069"
/tissue_type="degenerating cotyledons, 9-10 day old
etiolated seedling"
/lab_host="DH10B"
/note="vector: pBluescript II SK+; Site 1: EcoRI, Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

```

Query Match	13.1%	Score	34.2	DB	14	Length	536
Best Local Similarity	51.7%	Pred. No.	1.8				
Matches	78	Conservative	0	Mismatches	73		

QY	21	CCTTCACATCATTCTGTTATTTATATACCAATATATCCATGAGGCTCATATAAACAAGTCT	80
Db	269	CCTAGTCTTAGCTCCTCAATATAGTTCTCAAGAAGCAAAATGGCAATGGCATGGCACT	210
QY	81	TTCTCTTGGAAACAATGACCAAGATTGGGCAAAAGCTCTCCAAATGACATTTCAGCAAGG	140
Db	209	TTTCATCATGGAAAGCTAGAGCATATATGGGCAAAACCAAAACAGGGAATTCACCTCAAMGA	150
QY	141	AAAACATAAGACTCAAAGGCATTTATTATCCGG	171

Db 149 AGAACACAGATCAACGAATTCTTGTACACAGG 119

RESULT 12	BE661877/c	596 bp	EST 06-SEP-2000
LOCUS	BE661877	596 bp	
DEFINITION	6-C8 GmwxSC Glycine max cDNA, mRNA sequence.	1linear	
ACCESSION	BE661877		
VERSION	BE661877.1		
KEYWORDS	EST.		
SOURCE	soybean.		
ORGANISM	Glycine max		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 596)	Harris,N.,Chapman,B.P. and Gilzen,M.	Gene expression in developing soybean seed coats	Unpublished (2000)	Contact: Gilzen M

Agiculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@agr.ca

Location/Qualifiers
1. .596

```

/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_1lb="Gmaxsc"
/tissue_type="Seed coats"
/lab_host="E. coli strain XLOLR"
/notes="vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI. This
cDNA library was constructed from polyA+ enriched mRNA
from green seed coats in mid to late developmental stages
, average fresh weight 250 mg per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adapters were ligated to the
blunt-ended cDNA fragments and the products were digested
with XhoI for directional cloning into lambda ZAP Express
vector. This lambda library was amplified once using E.
coli host strain XL1 Blue MRF+. Inserts were then
subcloned by mass excision using Exassist helper phage for
conversion into phagemid vector PBK-CMV in E. coli host
strain XLOLR."

```

Query Match	13.1%	Score 34.2;	DB 10;	Length 596;
Best Local Similarity	51.7%;	Pred. No. 1.9;		
Matches 78; Conservative	0;	Mismatches 73.	Indels 0	

[illegible]

RESULT 13	LOCUS	DEFINITION	475 bp	mRNA	linear	EST 04-DEC-2001
BE36444/c	BE36444	sp25f04.y1 Gm-c1042 Glycine max	cdna	clone	GENOME	SYSTEMS CLONE ID.

Tue Dec 10 10:51:34 2002

us-09-880-457-1_copy_486_746.rst

Page 8

COMMENT

(E-mail: chimpbes@gsc.riken.go.jp,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.
PRIMERS

Sequencing: -21M13
LIBRARY

FEATURES
Source

```
Vector      : PKS145
R.Site 1    : SacI
R.Site 2    : SacI.
```

R.Site 2 : SacI.

R.Site 2 : SacI.

Location/Qualifiers
1: 1631

1. .631

```
/organism="Pan troglodytes"  
/db_xref="taxon:9598"
```

```
/db_xref="taxon:9598"
/cclone="PTR-144T17 F"
```

```
/clone="PTB-144I17.F"
```

```
sex="male"
```

```
/cell_type="lymphoblast"
/cclone_lib="PTA Chimeric"
```

Age	Sex	Occupation	Library
148	c	98 g	202 t
			2 others

[illegible]

ORIGIN

Query Match
Best Top

Best Local Similarity	13.0%;	Score 34;	DB 17;	Length 631;
	57.5%;	Pred. No. 2	3.	

Best Local Similarity	57.5%;	Pred. No. 2.3;
Matches	61;	Conservative
	0;	Mismatches

QY 39 ATTAATACCATCAATATCCCATGAGGCTCATAAACGAGTCTTTCTTCCTCCTCCCTCTCTCT

233
ATTAAATACCGGATTTTCTGGAACATGA 98

.....CAATTCATTAACCAAGTCTATAAAATGGAATGATGA 174

39 CCAAGATTTGGGCAACGCTCTCCAACATGACTTTCAGCAACGAAAA 144

```
Search completed: December 8, 2002, 19:27:07
Job time : 589.736 secs
```

Job time : 589.736 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:14 ; Search time 74.3192 Seconds
(without alignments)
7908.746 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atcgcaatcctgaacgtcag.....gttaattgagatcattcac 261

Scoring table: IDENTITY_NUC
Gapox 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251	96.2	1186	24	ABK33576
2	121.2	46.4	741	19	AAV69899
3	121.2	46.4	954	19	AAV69887
4	121.2	46.4	954	19	AAV41378
5	121.2	46.4	954	19	AAV41372
6	121.2	46.4	954	22	AAV41371
7	121.2	46.4	954	22	AAV41371
8	121.2	46.4	954	22	AAV41371
9	121.2	46.4	1945	24	ABK12877

10	121.2	46.4	2226	24	ABK12876	CDNA encoding huma
11	121.2	46.4	2271	19	AAZ9964	DNA encoding a hum
12	121.2	46.4	2274	21	AAV70285	Human osteoprotege
13	121.2	46.4	2390	24	ABK40274	CDNA encoding huma
14	118	45.2	1823	20	AAH80223	Human TRANCE encod
15	102	39.1	957	22	AAH6481	Rat osteoclast dif
16	95.6	36.6	735	19	AAV69898	Nucleic acid encod
17	95.6	36.6	951	19	AAV69900	Nucleic acid encod
18	95.6	36.6	951	21	AAZ99156	Mouse OBK nucleoti
19	95.6	36.6	951	21	AAZ99965	DNA encoding a mur
20	95.6	36.6	951	21	AAZ99024	Osteoclast formati
21	95.6	36.6	1538	19	AAV69886	Nucleic acid encod
22	95.6	36.6	1574	22	AAH25526	Nucleotide sequenc
23	95.6	36.6	1630	19	AAV41377	NF-KB receptor act
24	95.6	36.6	1630	19	AAV41371	NF-KB receptor act
25	95.6	36.6	1630	22	AAV41371	Murine receptor ac
26	95.6	36.6	1630	22	AAV41371	Murine receptor ac
27	95.6	36.6	1630	22	AAV41371	Murine RANKL (reco
28	95.6	36.6	2191	19	AAV41489	Nucleotide sequenc
29	95.6	36.6	2237	20	AAV41489	Murine TRANCE enco
30	95.6	36.6	2237	24	ABK12880	CDNA encoding mous
31	95.6	36.6	2295	19	AAV70284	Human osteoprotege
32	95.6	36.6	2299	21	AAZ99966	DNA encoding a mur
33	91	34.9	522	22	AAZ99966	Mouse OBK nucleoti
34	81.6	31.3	2029	21	AAZ99155	DNA encoding a syn
35	73.6	28.2	519	21	AAZ99968	DNA encoding a syn
36	73.6	28.2	519	21	AAZ99969	DNA encoding a mur
37	73.6	28.2	519	21	AAZ99972	DNA encoding osteo
38	73.6	28.2	546	21	AAZ99971	DNA encoding osteo
39	73.6	28.2	564	21	AAZ99967	DNA encoding a syn
40	73.6	28.2	564	21	AAZ99970	DNA encoding osteo
41	63	24.1	519	21	AAZ99973	DNA encoding osteo
42	36.2	13.9	2240	20	AAZ99973	CDNA sequence SEO
43	36.2	13.9	2291	20	AAZ99973	CDNA sequence SEO
44	36.2	13.9	3405	20	AAZ99973	CDNA sequence SEO
45	35.2	13.5	351	23	ABV23301	Human prostate exp

ALIGNMENTS

RESULT 1
ABK33576
ID ABK33576 standard; CDNA: 1186 BP.
AC ABK33576;
XX
DT 08-MAY-2002 (first entry)
XX
DE CDNA encoding human PRO protein, Seq ID No 81.
XX
KW Human: secreted protein; PRO: tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.

Db 320 GTTCCCTAAAGAGTCTGCTCTGTTGTAACATGATCGGGGTTGGCCAAAGATCTCCA 379
 Oy 122 ACATGACTTTCAGCAGCAAGAACTAAGAGTCA-----AAGCATTTTATTACCGGAATG 175
 Db 380 ACATGACTTTTAGAGAAAGAACTAATAGTAAATCAGATGGCTTTATTACCTGTATG 439
 Oy 176 CCGACATTTGCTCTGACATCGCGTAACCTGACAGCGCTTACTGTGACAGACCTTCACG 235
 Db 440 CCAACATTTGCTTTCGACATCATGAACTTCGAGAGACCTAGCTACAGAGTATCTTCAAC 499
 Oy 236 TA 237
 Db 500 TA 501
 RESULT 3
 AAV69887 standard: cDNA to mRNA; 954 BP.
 AC AAV69887;
 DT 10-FEB-1999 (first entry)
 XX Nucleic acid encoding a human OCIF-binding molecule (OBM).
 DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KM human; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /*tag= a
 XX
 PN MO9846644-A1.
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 DR WPI: 1998-594563/50.
 DR P-PSDB; AAW63018.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PT
 PS Claim 38; Page 115; 151pp; Japanese.
 XX
 CC The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone

CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 SQ Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other:
 Query Match 46.4%; Score 121.2; DB 19; Length 954;
 Best Local Similarity 74.8%; Pred. No. 1.5e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 Oy 4 GCAATCCTGACGCTCAGCCCTCAACATCATCTTGTATTATATACATCAATATCCATGAG 63
 Db 473 GCAAGCTGAAGCTCAGCCTTGTGCTCATCTCACTATTATATGCAACGACATCCCATGTG 532
 Oy 64 GCT--CATAAAGAGAGTCTTCTTCTTGAACATGACCAAGATTGGGCAACAGTCTCCA 121
 Db 533 GTTCCCTAAAGAGAGTCTGCTCTGTGTAACATGATCGGGGTGGCCAAAGATCTCCA 592
 Oy 122 ACATGACTTTCAGCAGCAAGAACTAAGAGTCA-----AAGCATTTTATTACCGGAATG 175
 Db 593 ACATGACTTTTAGCAATGAAACTAATAGTTAATCAGAGATGCTTTATTACCTGTATG 652
 Oy 176 CCGACATTTGCTCTGACATCGCGTAACCTGACAGAGCGCTTACTGTGACAGACCTTCACG 235
 Db 653 CCAACATTTGCTTTCGACATCATGAACTTCGAGAGACCTAGCTACAGAGTATCTTCAAC 712
 Oy 236 TA 237
 Db 713 TA 714
 RESULT 4
 AAV41378 standard: cDNA; 954 BP.
 ID AAV41378
 AC AAV41378;
 DT 08-OCT-1998 (first entry)
 XX
 DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /*tag= a
 FT /product= "human RANKL (ligand for RANK)"
 XX
 PN MO9828426-A2.
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US23775.
 XX
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 DR WPI: 1998-377657/32.
 DR P-PSDB; AAW69957.
 PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells
 XX

PS Claim 25; Pages 59-60; 80pp; English.

XX This cDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other.

SO Query Match 46.4%; Score 121.2; DB 19; Length 954;
Best Local Similarity 74.8%; Pred. No. 1.5e-30;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCGACCGCTTACCTTCACTGTTGTTATTAATACCATCAATATCCCATGAG 63
DB 473 GCACCTTGAACTGACCTGCTTGTGCTCACTCATATATGACGACATCCCATCTG 532
QY 64 GCT--CATAAACGAGTCTTCTTCTGGAACATGACCAAGATTGGCCAAACCTTCCA 121
DB 533 GTTCCCATTAAGTGAAGTCTGCTCTTGGTACCATGATGGGGTGGCCAAAGTCTCA 592
QY 122 ACATGACTTTTCGACCAAGCAAACTAAGAGTCA-----AAGCATTTTATTAACCGAATG 175
DB 593 ACATGACTTTTGAAGCAATGGAAGAACTAATAGTTATACGATGGCTTTTATTAACCTGATG 652
QY 176 CCGACATTTGCTTGCATCGCATCGCTACCTCAGCAGGCTTAACCTGACAGACCTTCAGC 235
DB 653 CCAACATTTGCTTGCATCGCATCGAATCTTCAAGAGACCTACAGATATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 5
AAV41372
ID AAV41372 standard; cDNA: 954 BP.
AC AAV41372;
XX
XX 08-OCT-1998 (first entry)
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
XX RANK: necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..954
FT CDS /*tag= a
FT /product= "human RANKL (ligand for RANK)"
XX
XX WO9828424-A2.
XX

PD 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23866.
XX
XX 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMM) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
PI WPI: 1998-377655/32.
XX
XX P-PSDB; AAM68293.
XX
XX New isolated receptor activator of necrosis factor-kappa B - useful
PT for, e.g. developing products for regulating an immune or
PT inflammatory response, treating toxic shock or sepsis
PS
PS Example 7; Pages 59-60; 80pp; English.

CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. Host cells transformed
CC or transfected with an expression vector comprising the RANK encoding
CC nucleic acid can be used to produce recombinant RANK protein. The soluble
CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC used for regulating an immune or inflammatory response. Inhibition of
CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC of an inflammatory response that result from triggering of RANK, e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC inflammatory reactions. They can also be used in adjunct therapy for
CC disease characterised by neoplastic cells that express RANK. The products
CC can also be used for detection and drug screening.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other.

SO Query Match 46.4%; Score 121.2; DB 19; Length 954;
Best Local Similarity 74.8%; Pred. No. 1.5e-30;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCGACCGCTTACCTTCACTGTTGTTATTAATACCATCAATATCCCATGAG 63
DB 473 GCACCTTGAACTGACCTTGTGCTCACTCATATTAAGCAACGACATCCCATCTG 532
QY 64 GCT--CATAAACGAGTCTTCTTCTGGAACATGACCAAGATTGGCCAAACGCTTCCA 121
DB 533 GTTCCCATTAAGTGAAGTCTGCTCTTGGTACCATGATGGGGTGGCCAAAGATCTCA 592
QY 122 ACATGACTTTTCGACCAAGCAAACTAAGAGTCA-----AAGCATTTTATTAACCGAATG 175
DB 593 ACATGACTTTTGAAGCAATGGAAGAACTAATAGTTATACGATGGCTTTTATTAACCTGATG 652
QY 176 CCGACATTTGCTTGCATCGCATCGCTACCTCAGCAGGCTTAACCTGACAGACCTTCAGC 235
DB 653 CCAACATTTGCTTGCATCGCATCGAATCTTCAAGAGACCTACAGATATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 6
AAD15311
ID AAD15311 standard; cDNA: 954 BP.
AC AAD15311;
XX
XX 15-NOV-2001 (first entry)
DE Human receptor activator of NF kappaB ligand (RANKL) cDNA.
XX
XX

XX Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..954 /tag= a
 FT /product= "Human RANK ligand (RANKL) protein"
 PN US6271349-B1.
 XX 07-AUG-2001.
 PD
 XX 17-DEC-1998; 98US-0215649.
 PF
 XX 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0772330.
 PR 07-MAR-1997; 97US-0813509.
 PR 22-DEC-1997; 97US-0996139.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Dougal1 WC, Galibert L;
 XX
 DR WPI: 2001-520313/57.
 DR P-PSDB; AAE08738.
 XX
 PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for
 PT regulating immune response, in screening for RANK inhibitors, or as an
 PT adjunct therapy for disease characterized by neoplastic cells that
 PT express RANK -
 XX
 PS Example 7; Column 69-71; 47pp; English.

SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
 Query Match 46.4%; Score 121.2; DB 22; Length 954;
 Best Local Similarity 74.8%; Pred. No. 1.5e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCATCCTGACGCTCAGCCCTTCACTCTTGTATTATATACATCAATATCCATGAG 63
 DB 473 GCATGCTGAAAGCTCAGCCCTTTGCTCATCTCACTATTATATGACACGACATCCACTG 532
 QY 64 GCT-CATAAAGAGATCTTCTTCTTGGAACATGACCAAGATTGGCAACGCTTCCA 121
 DB 533 GTTCCCATTAAGAGAGCTGCTCCCTTGATACCATGATCGGGGTTGGCCCAAGATCTCCA 592
 QY 122 ACATGACTTTCAGCAGCAAGAAACTAAGAGCA-----AAGGATTTATACCGGAATG 175
 DB 593 ACATGACTTTCAGCAGCAAGAAACTAAGAGCA-----AAGGATTTATACCGGAATG 175
 QY 176 CCGACATTTGCTCTCGCATCGGTAACTCAGCAGGCTTAACCTCAGGACCTTCAGC 235
 DB 653 CCAACATTTGCTCTTCGACATCATGAAGAACTTCAGGAGACCTAAGATATCTTCAAC 712
 QY 236 TA 237
 DB 713 TA 714
 XX
 RESULT 7
 AD08715
 ID AAD08715 standard; cDNA: 954 BP.
 XX
 AC AAD08715;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human receptor activator of NF- χ B ligand (hRANKL) cDNA.
 KW Human: receptor activator of NF- χ B; RANK; tumour necrosis factor; TNF;
 KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
 KW chromosome 18q22.1; hRANKL; chromosome 19q14; transmembrane protein; ss.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..954 /tag= a
 FT /product= "Human RANKL protein"
 FT
 PN US6242213-B1.
 XX
 PD 05-JUN-2001.
 PF
 XX 22-DEC-1997; 97US-0995659.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM;
 XX
 DR WPI: 2001-407216/43.
 DR P-PSDB; AAE04426.
 XX
 PT New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF- χ B
 PT receptor activator) of the receptor activator of NF- χ B (RANK) -
 XX
 PS Claim 2; Column 61-64; 43pp; English.
 XX
 CC The present invention relates to receptor activator of NF- χ B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to

OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	misc-feature
FT	81..131
FT	/tag= a
FT	/note= "tumour necrosis factor (ligand) superfamily,
FT	member 11 (TNFSF11), Specifically claimed in
FT	claim 4"
FT	
FT	misc-feature
FT	81..140
FT	/tag= b
FT	/note= "target region for antisense nucleic acid"
FT	CDS
FT	95..829
FT	/tag= c
FT	/product= "Human TRANCE (tumour necrosis factor-related
FT	activation induced cytokine) protein,
FT	splice variant 2"
PN	
XX	WO200216551-A2.
PD	
XX	28-FEB-2002.
PF	
XX	20-AUG-2001; 2001WO-US26101.
PR	
XX	18-AUG-2000; 2000US-226197P.
PA	(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
PI	
XX	Choi Y, Odgren PR, Marks SC:
DR	
XX	WPI: 2002-304119/34.
DR	P-PSDB; AAU78286.
PT	Treating mammal having disorder characterised by abnormal
PT	cartilage/skeletal growth such as dwarfism, acromegaly, by
PT	administering tumour necrosis factor-related activation induced
PT	cytokine-modulating agent to mammal -
XX	
XX	Disclosure; Fig 3; 55pp; English.
CC	The present invention relates to a new method of treating a mammal
CC	having a disorder comprising insufficient or excessive cartilage or
CC	skeletal growth. The method of the invention involves administering to
CC	the mammal a tumour necrosis factor-related activation induced cytokine
CC	(TRANCE)-modulating agent. The method is useful for treating a mammal
CC	having a disorder comprising insufficient or excessive cartilage or
CC	skeletal growth, where the disorder comprising insufficient cartilage
CC	or skeletal growth is selected from dwarfism, osteopetrosis,
CC	craniofacial-skeletal discrepancies and bone or cartilage damage
CC	resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
CC	arthritis, and disorders comprising excessive cartilage or skeletal
CC	growth are selected from acromegaly, gigantism, exostosis, carilagene,
CC	exostosis bursata and multiple osteochondroblastoma exostoses. The method
CC	is useful for inhibiting chondrocyte differentiation. The present
CC	nucleic acid sequence encodes the human TRANCE protein, splice variant
CC	2, of the invention. TRANCE is a member of the tumour necrosis factor
CC	family and acts directly on cartilage-producing cells (chondrocytes).
XX	
SQ	Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other:
	Query Match 46.4%; Score 121.2; DB 24; Length 1945;
	Best Local Similarity 74.8%; Pred. No. 2e-30;
	Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
OY	
DG	4 GCAATCGAGCCTTACACTTCATTATTAATACCATGCATATGCCATGAG 63
DB	GGAAGCTTGAACTAGCCTTTGTGCATCTCATTTAATATCCACGCAATCCATTCG 407
OY	64 GCT--CATAAAAGCATCTTTCTTTGGAAACATGACCACGATTTGGGCAACGCTCCA 121
DB	408 GTTCCCATTAATAATAGTAGTGTCTCTTGTGTACCATGATGGGGGTTGGGCAAGATCTCCA 467
OY	122 ACATGACTTTACGACAACGAAAACTAAGAGTCA-----AAGGCAATTTATTCGGGATG 175

Db	468	ACATGACCTTTAGCAATGAAACATAATAGTTAATCAGGATGGCTTTTATTACCTGTATG	527
Qy	176	CCGACATTTGCTCGACATCGCTACCTCAGAGGCGTAACCTGACGACCTTCAGC	235
Db	528	CCACATTTGCTTCGACATCATGATAAACTTCAGGAGCCTAGCTACAGAGTATCTTCAAC	587
Qy	236	TA 237	
Db	588	TA 589	
RESULT 10			
ABK12876			
ID	ABK12876	standard; cDNA; 2226 BP.	
XX	ABK12876;		
Dt	18-JUN-2002	(first entry)	
XX			
DE	cDNA encoding human TRANCE protein splice variant 1.		
XX			
KW	Human; tumour necrosis factor-related activation induced cytokine;		
KW	TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;		
KW	bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;		
KW	rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;		
KW	exostosis bursa; multiple osteochondilaginous exostosis; chondrocyte;		
KW	cartilage growth; skeletal growth; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	misc.feature	141..190	
FT	/tag= a		
FT	/note= "Tumour necrosis factor (ligand) superfamily,		
FT	member 11 (TNFSF11), target region for antisense		
FT	nucleic acid. Specifically claimed in claim 4"		
FT	CDS	157..1110	
FT	/tag= b		
FT	/product= "Human TRANCE (tumour necrosis factor-related		
FT	activation induced cytokine) protein,		
FT	splice variant 1"		
XX			
XX	WO200216551-A2.		
XX			
XX	28-FEB-2002.		
PD			
XX	20-AUG-2001; 2001WO-US26101.		
PF			
XX	18-AUG-2000; 2000US-226197P.		
PR			
XX			
PA	(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.		
XX			
PI	Choi Y, Odgren PR, Marks SC;		
XX			
DR	WPI; 2002-304119/34.		
DR	P-PSDB; AAU78285.		
PT	Treating mammal having disorder characterised by abnormal		
PT	cartilage/skeletal growth such as dwarfism, acromegaly, by		
PT	administering tumour necrosis factor-related activation induced		
PT	cytokine-modulating agent to mammal -		
XX			
PS	Disclosure; Fig 1; 55pp: English.		
XX			
CC	The present invention relates to a new method of treating a mammal		
CC	having a disorder comprising insufficient or excessive cartilage or		
CC	skeletal growth. The method of the invention involves administering to		
CC	the mammal a tumour necrosis factor-related activation induced cytokine		
CC	(TRANCE)-modulating agent. The method is useful for treating a mammal		
CC	having a disorder comprising insufficient or excessive cartilage or		
CC	skeletal growth, where the disorder comprising insufficient cartilage or		
CC	skeletal growth is selected from dwarfism, osteopetrosis,		

CC craniofacial-skeletal discrepancies and bone or cartilage damage
 CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
 CC arthritis, and disorders comprising excessive cartilage or skeletal
 CC growth are selected from acromegaly, gigantism, exostosis, caliclinea,
 CC exostosis bursata and multiple osteocartilaginous exostoses. The method
 CC is useful for inhibiting chondrocyte differentiation. The present
 CC nucleic acid sequence encodes the human TRANCE protein, splice variant
 CC 1, of the invention. TRANCE is a member of the tumour necrosis factor
 CC family and acts directly on cartilage-producing cells (chondrocytes).
 XX
 S0 Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;

Query Match 46.4%; Score 121.2; DB 24; Length 2226;
 Best Local Similarity 74.8%; Pred. No. 2.1e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACGCTTCACTCATCTGTTATTATACCATCAATATCCCATGAG 63
 DB 629 GCACGCTTGAAGCTGAGCTTTTGGTCATCTCATTTATGCGACCATCCCATCTG 688
 QY 64 GCT--CATAAACGAGTCTTCTTCTTGGAACATGACCAAGATGGGCAAGCTCCCA 121
 DB 689 GTTCCCATTAATAGTGTCTGCTCTTGTACCATGATGGGGTTGGCCAAAGATCTCCA 748
 QY 122 ACATGACTTTCAGCAACGAGAAACTAAGATCA-----AAGGCATTATTACCGGATG 175
 DB 749 ACATGACTTTCAGCAACGAGAAACTAAGATCAAGATGCGCTTTTATTACTGTATG 808
 QY 176 CCGACATTGCTCTGCATATCGGCTAAGCTCAGAGGCTTAAGTCTGACAGAGCTTCAGC 235
 DB 809 CCACGATTGCTTTCGACATCATGAACTTCAGAGAGCCTAGCTACAGAGTATCTTCAAC 868
 QY 236 TA 237
 DB 869 TA 870

RESULT 11
 AA299964
 ID AA299964 standard; DNA; 2271 BP.

XX AA299964;
 XX 25-JUL-2000 (first entry)

XX DNA encoding a human osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 185..1138
 FT /*tag= a
 FT /product= "osteoprotegerin ligand"

XX W0200015807-A1.

XX 23-MAR-2000.

XX 13-SEP-1999; 99MO-DK00481.

XX 15-SEP-1998; 98DK-0001164.

XX 02-OCT-1998; 98OS-0102896.

XX (MEBI-) M & E BIOTECH AS.

XX Halkier T, Haaning J;

XX WPI; 2000-271444/23.

DR P-PSDB; AAY84417.

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -
 FT
 XX

PS Disclosure; Page 75-77; 110pp; English.

XX The present sequence encodes a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 XX

S0 Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;

Query Match 46.4%; Score 121.2; DB 21; Length 2271;
 Best Local Similarity 74.8%; Pred. No. 2.1e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACGCTTCACTCATCTGTTATTATACCATCAATATCCCATGAG 63
 DB 657 GCACGCTTGAAGCTGAGCTTTTGGTCATCTCATTTATGCGACCATCCCATCTG 716
 QY 64 GCT--CATAAACGAGTCTTCTTCTTGGAAACATGACCAAGATGGGCAAGCTCTCA 121
 DB 717 GTTCCCATTAATAGTGTCTGCTCTTGTACCATGATGGGGTTGGCCAAAGATCTCCA 776

QY 122 ACATGACTTTCAGCAACGAGAAACTAAGATCA-----AAGGCATTATTACCGGATG 175
 DB 777 ACATGACTTTCAGCAACGAGAAACTAAGATCAAGATGCGCTTTTATTACTGTATG 836
 QY 176 CCGACATTGCTCTGCATATCGGCTAAGCTCAGAGGCTTAAGTCTGACAGAGCTTCAGC 235
 DB 837 CCACGATTGCTTTCGACATCATGAACTTCAGAGAGCCTAGCTACAGAGTATCTTCAAC 896

QY 236 TA 237
 DB 897 TA 898

RESULT 12
 AA70285
 ID AA70285 standard; DNA; 2274 BP.

XX AA70285;

XX 11-FEB-1999 (first entry)

XX Human osteoprotegerin binding protein from the pcDNA/nuOPGp1.insert.

XX Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODR;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 185..1138
 FT /*tag= a
 FT /product= "osteoprotegerin binding protein"

XX W09846751-A1.

PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98MO-US07584.
 XX
 PR 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 XX
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ;
 XX
 DR WPI; 1998-594578/50.
 DR P-PSDB; AAM63195.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 PS
 PS Claim 1; Fig 4; 47pp; English.
 XX
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 CC
 XX
 SQ Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
 Query Match 46.4%; Score 121.2; DB 19; Length 2274;
 Best Local Similarity 74.8%; Pred. No. 2.1e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCAATCCTGACGCTCAGCTTCACTCACTTGTATTATACCATCAATATCCCATGAG 63
 DB 657 GCAAGCTTGAAGCTCAGCTTGTGCTCACTCACTTATATATCCACCGACATCCACTG 716
 QY 64 GCT--CATTAACGAGCTTCTTCTTGTGAACATGACCAAGATTGGGAAAGCTGTCCA 121
 DB 717 GTTCCCATTAAGTAGTGTGCTTCTTGTGACCATGATGCGGTTGGCCACAGATTTCCA 776
 QY 122 ACATGACTTTGAGCAAGCAAGAACTAAGAGTCA-----AAGGCATTATTACCGGAATG 175
 DB 777 ACATGACTTTTAAAGCAAGAACTAATAGTAAATCAGATGCGCTTTTATTACCTGTATG 836
 QY 176 CCGACATTTGCTTGTGATGCGGTAACTTCAAGAGGCTTAATCTGCGAGGACTTCAAGC 235
 DB 837 CCAACATTTGCTTGTGATGATGAATCAAGTCAAGAGAGCTTAATCAAGTATCTTCAAC 896
 QY 236 TA 237
 DB 897 TA 898
 RESULT 13
 ABR40274
 ID ABR40274 standard; cDNA; 2390 BP.
 XX
 AC ABR40274;

XX
 DT 15-JUL-2002 (first entry)
 XX
 XX CDNA encoding human PRO206 polypeptide.
 DE
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cytostatic; neuroprotective; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153486-A1.
 PN
 PD 26-JUL-2001.
 PD
 PF 11-FEB-2000; 2000MO-US03565.
 PF
 PR 08-MAR-1999; 99MO-US05028.
 PR 11-MAR-1999; 99US-123972P.
 PR 11-MAY-1999; 99US-133459P.
 PR 02-JUN-1999; 99MO-US12252.
 PR 22-JUN-1999; 99US-140650P.
 PR 22-JUN-1999; 99US-140653P.
 PR 20-JUL-1999; 99US-144758P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 17-AUG-1999; 99US-149395P.
 PR 31-AUG-1999; 99US-151689P.
 PR 01-SEP-1999; 99MO-US20111.
 PR 15-SEP-1999; 99MO-US21090.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 01-DEC-1999; 99MO-US28634.
 PR 05-JAN-2000; 2000MO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
 PI Masters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-205567/26.
 DR P-PSDB; AA086148.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for
 PT treating benign or malignant tumours, leukemias and lymphoid
 PT malignancies, inflammatory, angiogenic and immunologic disorders -
 PS
 PS Claim 50; Fig 41; 302pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,
 CC bladder, breast, etc), leukemias and lymphoid malignancies, other
 CC disorders such as neuronal, glial, astrocytic, hypothalamic, glandular,
 CC macrophagal, stromal and blastocoele disorders, inflammatory, immune
 CC and angiogenic disorders. The polynucleotide sequences are also
 CC useful in gene therapy. ABR40254-ABR40288 encode for the human PRO
 CC polypeptides of the invention.
 CC
 XX
 SQ Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
 Query Match 46.4%; Score 121.2; DB 24; Length 2390;
 Best Local Similarity 74.8%; Pred. No. 2.2e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCAATCCTGACGCTCAGCTTCACTCACTTGTATTATTAATCAATATCCCATGAG 63
 DB 778 GCAAGCTTGAAGCTCAGCTTGTGCTCACTCACTTATTAATCCACCGACATCCACTG 837
 QY 64 GCT--CATTAACGAGCTTCTTCTTGTGAACATGACCAAGATTGGGAAAGCTGTCCA 121

Db 838 GTTCCCAATAAGTGAAGTCTGTCTTGGTACATGATCGGGGTTGGCAAGATCTCCA 897
 QY 122 ACATGACTTTCAGCAACGGAAGAACTAAGATCA-----AAGCATTATTATCCGGAATG 175
 Db 898 ACATGACTTTCAGCAACGGAAGAACTAAGATCAAGATGCGTTTATTACCTGTATG 957
 QY 176 CCGACATTTCCTCTGACATCGCTTAACCTCAGACAGGCTTAAGTCTCAGAGACCTTCAGC 235
 Db 958 CCAACATTTCCTCTGACATCATGAAACTTCAGAGACCTTAAGTCTCAGAGATATCTTCAC 1017
 QY 236 TA 237
 Db 1018 TA 1019

RESULT 14

AAX80223
 ID AAX80223 standard; cDNA; 1823 BP.
 AC AAX80223;

XX 17-AUG-1999 (first entry)
 DE Human TRANCE encoding cDNA.

XX TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
 KM TNF-related activation induced cytokine; immune response; cancer;
 KW autoimmune disease; HIV; hypersensitivity; allergen; ds.

XX Homo sapiens.

FH Key Location/Qualifiers
 FT CDS 1..738
 FT /tag= a

XX MO9929865-A2.

XX 17-JUN-1999.

XX 14-DEC-1998; 98WO-US26486.

XX 11-DEC-1998; 98US-0989479.

XX 12-DEC-1997; 97US-0989479.

XX 03-MAR-1998; 98US-0034099.

XX (UYRQ) UNIV ROCKEFELLER.

XX Choi Y, Josien R, Steinman R, Won B;

XX WPI: 1999-385609/32.

XX P-PSDB: AAY17873.

XX TNF like proteins for treating autoimmunity and cancer

XX Claim 1; Fig 1; 164bp; English.

XX The present sequence encodes human TNF-related activation induced
 CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
 CC variants, fragments, derivatives or analogues may be used as modulators
 CC of immune response in a mammal comprising, antisense sequences to
 CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
 CC Agonists and antagonists of TRANCE, can be used to modulate immune
 CC response by increasing or decreasing the life span of mature dendritic
 CC cells and increasing or decreasing T cell activation. These techniques
 CC are especially useful for treating immune system related conditions such
 CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.

CC The TRANCE polypeptides can be used to increase the viability of
 CC dendritic cells in vivo or in vitro, especially when used in conjunction
 CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
 CC CD40L or TNF-alpha).

XX Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

Query Match 45.2%; Score 118; DB 20; Length 1823;
 Best Local Similarity 74.0%; Pred. No. 2.3e-29;
 Matches 179; Conservative 0; Mismatches 55; Indels 8; Gaps 2;

QY 4 GCAATCCTGAGCGCTGAGCTTCATCATCTGTTATTTATATACCATATATCCATGAG 63
 Db 257 GCAACCTTGAAGCTAGACCTTTTGCATCTCAGTATATATGACACCGAATCCATCTG 316
 QY 64 GCT--CATAAAACGAGCTTTCCTTCCTTGGAAACATGACCAAGATTGGCAAAAGTCTCCA 121
 Db 317 GTTCCCATTAAGTGAAGTCTGTCTCTGTGTACCATGATGAGGGGTGGTAAGATCTCCA 376
 QY 122 ACATGACTTTCAGCAACGGAAGAACTAAGATCA-----AAGCATTATTATCCGGAATG 175
 Db 377 ACATGACTTTCAGCAACGGAAGAACTAAGATCAAGATGCGTTTATTACCTGTATG 436
 QY 176 CCGACATTTCCTCTGACATCGCTTAACCTCAGACAGGCTTAAGTCTCAGAGACCTTCAGC 235
 Db 437 CCAACATTTCCTCTGACATCATGAAACTTCAGAGACCTTAAGTCTCAGAGATATCTTCAC 496
 QY 236 TA 237
 Db 497 TA 498

RESULT 15

AAF86481
 ID AAF86481 standard; cDNA; 957 BP.

XX AAF86481;

XX 29-JUN-2001 (first entry)

XX Rat osteoclast differentiation factor, ODF, coding sequence.

XX Rat: osteoclast formation inducer; vaccine; gene therapy;

XX Osteoclast Differentiation Factor; bone; ss.

XX Rattus sp.

FH Key Location/Qualifiers
 FT CDS 1..957
 FT /tag= a
 FT /product= "Rat ODF"

XX WO200123549-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-AU01202.

XX 29-SEP-1999; 99AU-0003147.

XX (UYMA-) UNIV WESTERN AUSTRALIA.

XX Xu J, Zheng M;

XX WPI: 2001-335526/35.

XX P-PSDB: AAB82092.

XX Novel nucleic acid encoding rat osteoclast differentiation factor

XX useful for modulating activity of a cell, e.g., cell proliferation,

XX cell differentiation and cell viability -

XX Claim 1; Fig 1; 81bp; English.

XX The present sequence is the coding sequence for rat Osteoclast
 CC Differentiation Factor (ODF). ODF is thought to be directly involved in
 CC the differentiation of monocytes/macrophages into osteoclasts.
 CC Osteoclasts promote dissolution of the bone matrix and solubilisation of
 CC bone salts. The present sequence is useful in gene therapy, and as
 CC hybridisation probes or primers. ODF protein is useful for modulating the

CC activity of cells, e.g., cell proliferation, cell differentiation and
cell viability, as immunogens to generate anti-rat ODF antibodies, and
as vaccines. Anti-rat ODF antibodies are useful in assay methods for
quantifying ODF polypeptides.

XX
SQ Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other;

Query Match 39.1%; Score 102; DB 22; Length 957;
Best Local Similarity 69.8%; Pred. No. 4.4e-24;

Matches 169; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

```
QY 3 GGCATTCCTGACGCTGCGCTTCACTCATCTTGTATTATACCATCAATATCCCATGA 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 475 GGCACGCTGAGGCTGAGCGCTTGTCTCACCCTCACCATCATGCTGCCGACATCCCATCG 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 GG--CTCATTAAGAGAGTCTTTCTTGGAAACATGACCAAGATTGGCAACGCTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 535 GGTTCCTAATAAGTCAAGTCTGTCTCTTGGTACCATGATGAGGCTGGCCAGATCTCT 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 AACATGACTTTGAGCAAGGAAAACTAAGATCA-----AAGCATTTATTACCGAAT 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 595 AACATGACGTTAAGCAACGAAAACTAAGGTTAACCAAGATGGCTTCTATTACCTGTAC 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 GCCGACATTGCTCTGACATCGGCTAACCTCAGCAGGCTTAAGTCTGACAGACCTCAG 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 655 GCCAACATTTGCTTCAAGCATCATGAACCTCAGGAGCGTACCTGCCGACTATCTTCAG 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 CT 236
    ||
DB 715 CT 716
```

Search completed: December 8, 2002, 17:26:15

Job time : 81.3192 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 16:41:40 ; Search time 558.919 Seconds
(without alignments) 13590.225 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746
Sequence: 1 atggcaatcctgacgcctcag.....gtaattgagaatcattcac 261

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ha:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_wa:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_or:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rnd:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	251	96.2	1186	6	AX358828
2	251	96.2	1186	6	AX362321
3	249.4	95.6	165707	2	AC104794
4	249.4	95.6	190748	9	AC010969
5	121.2	46.4	818	9	AB064268
6	121.2	46.4	911	9	AB061227
7	121.2	46.4	930	9	AB037599
8	121.2	46.4	954	6	AR156434
9	121.2	46.4	954	6	AR164148
10	121.2	46.4	954	6	AX147989
11	121.2	46.4	954	6	AX451895
12	121.2	46.4	972	9	AB064270
13	121.2	46.4	1034	9	AB064269
14	121.2	46.4	2201	9	AF019047
15	121.2	46.4	2271	6	AF053712
16	121.2	46.4	2290	6	AX201362
17	118	45.2	1823	9	AF013171
18	102	39.1	957	10	AF187319
19	97.8	37.5	113451	2	AC023297
20	97.8	37.5	200724	9	AL139382
21	95.6	36.6	754	10	AB032772
22	95.6	36.6	864	10	AB032771
23	95.6	36.6	951	6	E34350
24	95.6	36.6	951	6	E34350
25	95.6	36.6	951	10	AB008426
26	95.6	36.6	951	10	AB008426
27	95.6	36.6	1630	6	AR156433
28	95.6	36.6	1630	6	AR164147
29	95.6	36.6	1630	6	AX147987
30	95.6	36.6	1694	6	AX451897
31	95.6	36.6	2191	6	AR157058
32	95.6	36.6	2191	6	AX140162
33	95.6	36.6	2225	10	AF019048
34	95.6	36.6	2237	10	AF013170
35	95.6	36.6	2295	6	AR062119
36	95.6	36.6	2299	10	AF053713
37	91	34.9	522	6	AX232589
38	84.8	32.5	127812	2	AC094149
39	81.6	31.3	2029	6	E34349
40	81.6	31.3	2029	10	AB022036S4
41	81.6	31.3	276831	2	AC126690
42	37.2	14.3	142588	2	AC023297
43	37	14.2	113451	9	AC007716
44	36.8	14.1	169759	9	AC007716
45	36.8	14.1	169960	9	AC006440

ALIGNMENTS

RESULT 1
AX358828 1186 bp DNA linear PAT 13-FEB-2002
LOCUS AX358828
DEFINITION Sequence 81 from Patent WO0193983.
ACCESSION AX358828
VERSION AX358828.1 GI:18675315
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: WO 0193983-A 81 13-DEC-2001;
 FEATURES Genentech Inc. (US)
 SOURCE Location/Qualifiers
 1. 1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 96.2%; Score 251; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 2.4e-68;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTTATTAATACCATATATCCAT 60
 |||||||
 DB 447 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTTATTAATACCATATATCCAT 506
 |||||||

QY 61 GAGGCTCTAAAGAGAGCTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 120
 |||||||
 DB 507 GAGGCTCTAAAGAGAGCTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 566
 |||||||

QY 121 AACATGACTTCAGCAAGCAAACTAGAGTCAAGCATTTATTTACCGGAATGCCGAC 180
 |||||||
 DB 567 AACATGACTTCAGCAAGCAAACTAGAGTCAAGCATTTATTTACCGGAATGCCGAC 626
 |||||||

QY 181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGCCTTCAGTATAG 240
 |||||||
 DB 627 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGCCTTCAGTATAG 686
 |||||||

QY 241 TGTAAATTTGAG 251
 |||||||
 DB 687 TGTAAATTTGAG 697
 |||||||

RESULT 2
 AX362321 1186 bp DNA linear PAT 15-FEB-2002
 LOCUS Sequence 81 from Patent WO0208288.
 ACCESSION AX362321
 VERSION AX362321.1 GI:18694618
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 Baker, R.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 81 31-JAN-2002;
 FEATURES Genentech, Inc. (US)
 SOURCE Location/Qualifiers
 1. 1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 96.2%; Score 251; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 2.4e-68;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTTATTAATACCATATATCCAT 60
 |||||||
 DB 447 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTTATTAATACCATATATCCAT 506
 |||||||

QY 61 GAGGCTCTAAAGAGAGCTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 120
 |||||||
 DB 507 GAGGCTCTAAAGAGAGCTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 566
 |||||||

QY 121 AACATGACTTCAGCAAGCAAACTAGAGTCAAGCATTTATTTACCGGAATGCCGAC 180
 |||||||
 DB 567 AACATGACTTCAGCAAGCAAACTAGAGTCAAGCATTTATTTACCGGAATGCCGAC 626
 |||||||

QY 181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGCCTTCAGTATAG 240
 |||||||
 DB 627 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGCCTTCAGTATAG 686
 |||||||

QY 241 TGTAAATTTGAG 251
 |||||||
 DB 687 TGTAAATTTGAG 697
 |||||||

RESULT 3
 AC104794 165707 bp DNA linear HTG 30-APR-2002
 LOCUS Homo sapiens chromosome 2 clone RP11-254F7, WORKING DRAFT SEQUENCE,
 3 unordered pieces.
 DEFINITION
 AC104794
 AC104794.3 GI:20340520
 ACCESSION
 AC104794.3 GI:20340520
 VERSION
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 165707)
 AUTHORS
 Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 AUTHORS
 2 (bases 1 to 165707)
 WATERSTON, R.H.
 DIRECT SUBMISSION
 Submitted (21-DEC-2001) Genome Sequencing Center, Washington
 MO 63108, USA
 3 (bases 1 to 165707)
 WATERSTON, R.H.
 DIRECT SUBMISSION
 Submitted (30-APR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Apr 30, 2002 this sequence version replaced gi:19339129.

COMMENT

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 Contact: submissions@wustl.wustl.edu
 ----- Project Information -----
 Center project name: H_NH0254F07
 ----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 162662 bases at least Q40
 Consensus quality: 163189 bases at least Q30
 Consensus quality: 164786 bases at least Q20
 Insert size: 167795; agarose-fp
 Quality coverage: 12.78 in Q20 bases; agarose-fp
 Quality coverage: 10.53 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

```

* be preserved.
* 1 1112: contig of 1112 bp in length
* 1113 1212: gap of unknown length
* 1213 76227: contig of 75015 bp in length
* 76228 76327: gap of unknown length
* 76328 165707: contig of 89380 bp in length.
FEATURES
  source
    1..165707
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="2"
      /clone="RP11-2547"
  misc_feature
    1..1112
      /note="assembly_name:Contig21"
  misc_feature
    1213..76227
      /note="assembly_name:Contig68"
  misc_feature
    76328..165707
      /note="assembly_name:Contig69"
BASE COUNT  42887 a 42242 c 39083 g 41295 t 200 others
ORIGIN
Query Match      95.6%; Score 249.4; DB 2; Length 165707;
Best Local Similarity 99.6%; Pred. No. 7e-68;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGCAATCTGACGCTCACTGCTTCTTATATACATCATATCCCAT 60
    |||
DB 41120 ATGGCAATCTGACGCTCACTGCTTCTTATATACATCATATCCCAT 41179
    |||
QY 61 GAGGCTCATAAACGAGTCTTCTTGTGGAACATGACCAAGATTGGCAACGCTCTCC 120
    |||
DB 41180 GAGGCTCATAAACGAGTCTTCTTGTGGAACATGACCAAGATTGGCAACGCTCTCC 41239
    |||
QY 121 AACATGACTTTGACGACGGAAGAACTAGAGTCAAGGCAATTTATACCGGATGCCGAC 180
    |||
DB 41240 AACATGACTTTGACGACGGAAGAACTAGAGTCAAGGCAATTTATACCGGATGCCGAC 41299
    |||
QY 181 ATTTGCTCTGACATGCGGACCTGACGAGGCTTACTGACGACCTTACGCTATGG 240
    |||
DB 41300 ATTTGCTCTGACATGCGGACCTGACGAGGCTTACTGACGACCTTACGCTATGG 41359
    |||
QY 241 TGTATTTTGGAG 251
    |||
DB 41360 TGTATTTTGGAG 41370

```

```

RESULT 4
AC010969/c 190748 bp DNA linear PRI 07-NOV-2001
LOCUS Homo sapiens BAC clone RP11-95D17 from 2, complete sequence.
DEFINITION AC010969
ACCESSION AC010969.11 GI:13677120
VERSION
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
  AUTHORS Sulston, D.E. and Waterston, R.
  TITLE Toward a complete human genome sequence
  JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE 99063792
  PUBMED 9847074
REFERENCE
  2 (bases 1 to 190748)
  Sun, H., Abbott, A. and Le, T.P.
  TITLE The sequence of Homo sapiens BAC clone RP11-95D17
  JOURNAL Unpublished
  3 (bases 1 to 190748)
  Waterston, R.H.
  REFERENCE
    Direct Submission
    Submitted (28-SEP-1999) Genome Sequencing Center, Washington
    University School of Medicine, 4444 Forest Park Parkway, St. Louis,
    MO 63108, USA

```

```

REFERENCE
  AUTHORS Waterston, R.H.
  TITLE Direct Submission
  JOURNAL Submitted (19-APR-2001) Genome Sequencing Center, Washington
    University School of Medicine, 4444 Forest Park Parkway, St. Louis,
    MO 63108, USA
REFERENCE
  AUTHORS 5 (bases 1 to 190748)
  TITLE Direct Submission
  JOURNAL Submitted (20-APR-2001) Genome Sequencing Center, Washington
    University School of Medicine, 4444 Forest Park Parkway, St. Louis,
    MO 63108, USA
REFERENCE
  AUTHORS 6 (bases 1 to 190748)
  TITLE Direct Submission
  JOURNAL Submitted (07-NOV-2001) Department of Genetics, Washington
    University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
    On Apr 19, 2001 this sequence version replaced gi:1118441.
COMMENT
  ----- Genome Center
  Center: Washington University Genome Sequencing Center
  Web site: http://genome.wustl.edu/gsc
  Contact: saplens@wustl.wustl.edu
  ----- Summary Statistics
  Center project name: H.NH0095D17

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Fritgen, E., Tateno, M., Catanesi, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://backpac.med.buffalo.edu>)
VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-52D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17.

There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish RP11-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Size information from restriction digest suggests that the full repeat may not be represented.

```

FEATURES
  source
    1..190748
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="2"

```

```

/map="2"
/clone="Rp11-95D17"
/clone.lib="RPC1-11"
repeat_region 185..230
/rpt_family="L2"
323..805
/rpt_family="L1"
806..1114
/rpt_family="Alu"
1449..1567
/rpt_family="MIR"
2179..2369
/rpt_family="MIR"
2626..3646
/rpt_family="L2"
3716..3745
/rpt_family="AT-rich"
3798..4101
/rpt_family="Alu"
4196..5255
/rpt_family="L1"
5256..5559
/rpt_family="Alu"
5560..6453
/rpt_family="L1"
6939..6969
/rpt_family="MIR"
7701..8007
/rpt_family="Alu"
8242..8532
/rpt_family="MERL-type"
8533..8834
/rpt_family="Alu"
8835..9300
/rpt_family="MERL-type"
9322..9647
/rpt_family="L2"
9652..9784
/rpt_family="MALR"
9784..9848
/rpt_family="Alu"
9862..10061
/rpt_family="L1"
10062..10360
/rpt_family="Alu"
10361..10646
/rpt_family="L1"
10647..10948
/rpt_family="Alu"
10949..11090
/rpt_family="L1"
11135..11420
/rpt_family="Alu"
11424..11704
/rpt_family="L1"
11705..12015
/rpt_family="Alu"
12016..12045
/rpt_family="L1"
12047..12327
/rpt_family="Alu"
12335..12416
/rpt_family="L1"
12467..12594
/rpt_family="Alu"
12596..12678
/rpt_family="L1"
12698..12954
/rpt_family="Alu"
12955..13065
/rpt_family="Alu"
13194..13433
/rpt_family="L2"

```

```

repeat_region 13557..13667
/misc_feature 13614..14110
/misc_feature 13623..14122
/misc_feature 13630..14128
/misc_feature 13635..14128
/misc_feature 13688..13942
/misc_feature 13727..14127
/misc_feature 13729..14126
/misc_feature 13735..13801
/misc_feature 14062..14259
/misc_feature 14144..14259
/misc_feature 14205..14259
/misc_feature 14229..14259
/misc_feature 14422..14474
/misc_feature 14851..15156
repeat_region 14851..15156

```

Query Match
Best Local Similarity 95.68; Score 249.4; DB 9; Length 190748;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATGCAATCCTGAGCGAGCTTCACATCATCTTTATTAATACATCAATATCCAT 60
Db 174485 ATGCAATCCTGAGCGAGCTTCACATCATCTTTATTAATACATCAATATCCAT 174426
QY 61 GAGGCTATTAAGAGAGCTTTCTTTGGAACATGACCAAGATTGGCAAGCTGCC 120
Db 174425 GAGGCTATTAAGAGAGCTTTCTTTGGAACATGACCAAGATTGGCAAGCTGCC 174366
QY 121 AACATGACTTTCAGCAAGGAAAGAACTAAGAGTCAAGGCAATTAATCCGGAATGCCGAC 180
Db 174365 AACATGACTTTCAGCAAGGAAAGAACTAAGAGTCAAGGCAATTAATCCGGAATGCCGAC 174306
QY 181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCGCTTAACCTGCGAGGACCTATG 240
Db 174305 ATTTGCTCTCGACATCGCGTAACCTCAGCAGGCGCTTAACCTGCGAGGACCTATG 174246
QY 241 TGTAAATTGAG 251
Db 174245 TGTAAATTGAG 174235

```

```

RESULT 5
AB064268 818 bp mRNA linear PRI 26-DEC-2001
LOCUS Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor
DEFINITION kappa B ligand 3, complete cds.
ACCESSION AB064268
VERSION AB064268.1 GI:18143616
KEYWORDS Homo sapiens cDNA to mRNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 818)
AUTHORS Ikeda,T. and Kuroyama,H.

```

TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: toru.ph2@med.tmd.ac.jp, Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)

FEATURES Location/Qualifiers

source

1. .818
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .818
/gene="hRANKL 3"
84. .818
/gene="hRANKL 3"
/codon_start=1
/product="receptor activator of nuclear factor kappa B ligand 3"
/protein_id="BAB79693.1"
/db_xref="GI:18143617"
/translation="MDPNRISDGTGHCIVRIILRHENADFDPTLESODPKLIPDSOR RIKOAFQAVOKELQHTVSOHTRAEKAMVDGSLDAKSKLEAOPFAHTITATIT PDSGSHKVSLSWYHDSGMARISNMFTSNGKLVNODGFYLYANICFRHHTSGDLAT EYQLMYYVTIKSIKIPSSHTLMKGSSTKYWSGNSSEHFYSINVGFEFLKSGEISL EVSNPSLDDPDATYFGAFKVRID"

CDS

BASE COUNT 243 a 173 c 184 g 218 t
ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 818;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCGACGCTGACCTCACTCATCTGTATTAATCATCATATCCCATGAG 63
DB 337 GCAAGCTTGAAGCTAGCTTGTCTCATCTCATTTATATCCACGACATCCATCTG 396
QY 64 GCT--CATAAACGAGCTTTCTCTTGGAAACATGACCAAGATTGGGCAACGCTCCA 121
DB 397 GTTCCATTAAGTAGTGTCTCTTGGTACCATGATGGGGTGGCCAGATCTCCA 456
QY 122 ACATGACTTTGACGACGGAAGAACTAAGATCA-----AAGCATTTTATCCGGAATG 175
DB 457 ACATGACTTTGACGACGGAAGAACTAAGATCAAGATGAGATGCTTTATACCTGTATG 516
QY 176 CCGACATTTGCTCTGACATCGCTACCTCAGACAGGCTTAACCTGACGACCTTCAGC 235
DB 517 CCAACATTTGCTTTCGACATCATGAACCTTCAGAGACCTAGCTACAGATATCTTCAC 576
QY 236 TA 237
DB 577 TA 578

RESULT 6
AB061227 911 bp mRNA linear PRI 03-NOV-2001
LOCUS Homo sapiens mRNA for hRANKL 2, complete cds.
DEFINITION AB061227
ACCESSION AB061227.1 GI:16610212
VERSION
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Ikeda, T., Kuroyama, H. and Hirokawa, K.
TITLE Human RANKL Isoform
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 911)
AUTHORS Ikeda, T. and Kuroyama, H.
TITLE Direct Submission
JOURNAL Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.ph2@med.tmd.ac.jp,

FEATURES Location/Qualifiers
source 1. .911
/organism="Homo sapiens"
/db_xref="taxon:9606"
99. .911
/codon_start=1
/product="hRANKL 2"
/protein_id="BAB71768.1"
/db_xref="GI:15610213"
/translation="MEYALLGLGIGYVCSALFFYPRADMPNRISDGTGHCIVRI LRIHENADFDPTLESODPKLIPDSORRIKQAFQAVQREKHIVSOHTRAEKAMVDG SWDLAKRSKLEAOPFAHTITATIDIPSGHVSLSWYHDSGMARISNMFTSNGKLV NODGFYLYANICFRHHTSGDLATEYQLMYYVTIKSIKIPSSHTLMKGSSTKYWS GNSSEHFYSINVGFEFLKSGEISIEVSNPSLDDPDATYFGAFKVRID"

CDS

BASE COUNT 253 a 211 c 217 g 230 t
ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 911;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCGACGCTGACCTCACTCATCTGTATTAATCATCATATCCCATGAG 63
DB 430 GCAAGCTTGAAGCTAGCTTGTCTCATCTCATTTATATCCACGACATCCATCTG 489
QY 64 GCT--CATAAACGAGCTTTCTCTTGGAAACATGACCAAGATTGGGCAACGCTCCA 121
DB 490 GTTCCATTAAGTAGTGTCTCTTGGTACCATGATGGGGTGGCCAGATCTCCA 549
QY 122 ACATGACTTTGACGACGGAAGAACTAAGATCA-----AAGCATTTTATCCGGAATG 175
DB 550 ACATGACTTTGACGACGGAAGAACTAAGATCAAGATGAGATGCTTTATACCTGTATG 609
QY 176 CCGACATTTGCTCTGACATCGCTACCTCAGACAGGCTTAACCTGACGACCTTCAGC 235
DB 610 CCAACATTTGCTTTCGACATCATGAACCTTCAGAGACCTAGCTACAGATATCTTCAC 669
QY 236 TA 237
DB 670 TA 671

RESULT 7
AB037599 930 bp mRNA linear PRI 19-MAR-2002
LOCUS Homo sapiens mRNA for SODF/TRANCE, complete cds.
DEFINITION AB037599
ACCESSION AB037599.1 GI:6863047
VERSION
KEYWORDS
SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma cell line: SCC-4 cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Nagai, M., Kyakumoto, S. and Sato, N.
TITLE Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation
JOURNAL Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)

REFERENCE 2 (bases 1 to 930)
AUTHORS Nagai, M., Kyakumoto, S. and Sato, N.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchamaru, Morioka, Iwate 020-8505, Japan (E-mail: mnagai@iwate-med.ac.jp, Tel: +81-19-651-5111 (ex. 4436), Fax: +81-19-654-4147)

FEATURES Location/Qualifiers
source 1. .930
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

/sex="male"
/cell_line="SCC-4"
/tissue_type="epithelial-like squamous cell carcinoma"
1. 930
/gene="sodf/trance"
95. 829
/gene="sodf/trance"
/codon_start=1
/product="SODF/TRANCE"
/protein_id="AAA90488.1"
/db_xref="GI:5863048"
/translation="MDPNRISDGTGHCITRIILRHENADFDPTLESODPTKILPDSR
RIKAFQGAQVQKELQHVQSHIRAEKAMVDSMDLAKRSKLEAOPFAHLINADI
PSGSHKYSLSMVDHGRWAKISNMTFSGKLVNODGYYLYLVANTCFRRHETSGDIAT
EYDLMYVVTSTSIKIPSSHTLKGSGTKYKYSNGSEPHFYSINVGFRFLRSGEELIS
EVSNPDLDPDODATYFCAKFRVRIID"
BASE COUNT      283 a      184 c      200 g      260 t      3 others
ORIGIN

```

```

Query Match      46.4%; Score 121.2; DB 9; Length 930;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCTGACGCTCAGCCTTCACTCACTCTTGTATTAATACATCAATATCCATGAG 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 348 GCAAGCTTGAAGCTCAGCCTTTGCTCATCTCATATTAATGCCAGCATCCATCTG 407
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 GCT--CATAAAGAGTCTTCTCTTGGAACATGACCAAGATTGGGCAACGTCCTCA 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 408 GTTCCCATTAAGTAGTCTGTCTCTTGTACATGATGGGGTGGGCAAGATCTCCA 467
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 ACATGACTTTCAGCAGGAACTAAGAGTCA-----AAGCATTTATTAACCGAATG 175
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 468 ACATGACTTTAGCAATGAAGAACTAATAGTTAATCAGAGATGGCTTTATTAATCTGTATG 527
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 176 CCGACATTTGCTCTGACATCGCTTAACCTCAGCAGCCTTAACCTGACAGACCTTCAGC 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 528 CCACATTTGCTTTCGACATCATGAACTTCAAGAGACCTAGCAGATGATCTTCAAC 587
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 236 TA 237
    ||
DB 588 TA 589
    ||

```

```

RESULT 8
LOCUS      AR156434          954 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6242213.
ACCESSION  AR156434
VERSION     AR156434.1  GI:15125138
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 954)
AUTHORS    Anderson, D.M.
TITLE       Isolated DNA molecules encoding RANK-L
JOURNAL     Patent: US 6242213-A 12 05-JUN-2001;
FEATURES
    source          1..954
                     /organism="unknown"
BASE COUNT      255 a      239 c      227 g      233 t
ORIGIN

```

```

Query Match      46.4%; Score 121.2; DB 6; Length 954;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCTGACGCTCAGCCTTCACTCACTCTTGTATTAATACATCAATATCCATGAG 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 GCAAGCTTGAAGCTCAGCCTTTGCTCATCTCATATTAATGACAGACATCCATCTG 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

QY 64 GCT--CATAAAGAGTCTTCTCTTGGAACATGACCAGATGGGCAACGTCCTCA 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 533 GTTCCCATTAAGTAGTCTGTCTCTGTGACCATGATCGGGTGGCCAGATCTCCA 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 ACATGACTTTCAGCAGGAAACTAAGAGTCA-----AAGCATTTATTAACCGAATG 175
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 593 ACATGACTTTTACGACATGAAACTAATAGTTAATCAGATGCTTTTATTAACCTGTATG 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 176 CCGACATTTGCTCTGACATCGCGTAACTCAGCAGCCTTAACCTGACAGACCTTCAGC 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 653 CCACATTTGCTTTCGACATCATGAACTTCAAGAGACCTTACTACAGATATCTTCAAC 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 236 TA 237
    ||
DB 713 TA 714
    ||

```

```

RESULT 9
LOCUS      AR164148          954 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 12 from patent US 6271349.
ACCESSION  AR164148
VERSION     AR164148.1  GI:16235114
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 954)
AUTHORS    Dougal, W.C., and Galibert, L.
TITLE       Receptor activator of NF- $\kappa$ B
JOURNAL     Patent: US 6271349-A 12 07-AUG-2001;
FEATURES
    source          1..954
                     /organism="unknown"
BASE COUNT      255 a      239 c      227 g      233 t
ORIGIN

```

```

Query Match      46.4%; Score 121.2; DB 6; Length 954;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCTGACGCTCAGCCTTCACTCACTCTTGTATTAATACATCAATATCCATGAG 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 473 GCAAGCTTGAAGCTCAGCCTTTGCTCATCTCATATTAATGCCAGCATCCATCTG 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 GCT--CATAAAGAGTCTTCTCTTGGAACATGACCAGATGGGCAACGTCCTCA 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 533 GTTCCCATTAAGTAGTCTGTCTCTGTGACATGATCGGGTGGCCAAAGATCTCCA 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 ACATGACTTTCAGCAGGAACTAAGAGTCA-----AAGCATTTATTAACCGAATG 175
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 593 ACATGACTTTTACGACATGAAACTAATAGTTAATCAGATGCTTTTATTAACCTGTATG 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 176 CCGACATTTGCTCTGACATCGCGTAACTCAGCAGCCTTAACCTGACAGACCTTCAGC 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 653 CCACATTTGCTTTCGACATCATGAACTTCAAGAGACCTTACTACAGATATCTTCAAC 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 236 TA 237
    ||
DB 713 TA 714
    ||

```

```

RESULT 10
LOCUS      AX147989          954 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 12 from Patent WO0136637.
ACCESSION  AX147989
VERSION     AX147989.1  GI:14346964
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```


REFERENCE 1 (bases 1 to 954)
 AUTHORS Anderson, D.M. and Hughes, A.E.
 TITLE Receptor activator of nf-kappa b
 JOURNAL Patent: WO 0136637-A 12 25-MAY-2001.
 FEATURES
 source
 1. 954
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 CDS
 1..954
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="C4C41185.1"
 /translation="MRRASRDYTKYLRGSEMGGPGAPHEGLHAPPAPHPAPPA
 SSMFVALLIGIGVQVCSVALFFEPRAQMDPNRISDGTCHICIRILRLHFNADPDT
 TLESODTKLIPDSCKRIKQAFQCAVOKELQIIVSOHRAEKAMVDGMDLAKRSKL
 EADPFAHLITNADIPSGSHKVSLSWYHGRMAKISNMFTSNGKLIYNQDGYLYLA
 NICFRHETSGDLATEYLQIMVYVTKTSIKIPSSHTLMKGGSTRYWNSSEHFYSIN
 VGGFRLRSGEISIEVSNPSLDDPDQDARYFGAFKVRDID"

BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 46.4%; Score 121.2; DB 6; Length 954;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCGTCGACGCTCAGCCTCATCTGTTATTAATCATCATATCCCATGAG 63
 Db 473 GCAAGCTTGAAGCTCAGCTTTGCTCATCTCATCTATTATGCGCAGCATCCCATCTCG 532

QY 64 GCT--CATAAACGAGTCTTCTCTTGGAACATGACCAAGATTGGCGCAACGTCCTCA 121
 Db 533 GTTCCCATTAAGTAGTGTGCTGCTCATCTCATCTATTATGCGCAGCATCCCATCTCG 532

QY 122 ACATGACTTTCAGCAAGCAAACTAGAGTCA-----AAGGCATTATTACCGGAATG 175
 Db 593 ACATGACTTTCAGCAAGCAAACTAGAGTCA-----AAGGCATTATTACCGGAATG 652

QY 176 CCGACATTTGCTCGACATCGGCTTAACCTGAGGCTTACCTGCGAGACCTTCAGC 235
 Db 653 CCAACATTGCTTTCGACATCGGCTTAACCTGAGGACCTTACCTGAGATCTTCAAC 712

QY 236 TA 237
 Db 713 TA 714

RESULT 11
 AX451895 954 bp DNA linear PAT 03-JUL-2002
 LOCUS Sequence 5 from Patent W00224896.
 DEFINITION AX451895
 ACCESSION AX451895
 VERSION AX451895.1 GI:21698735
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Dougall, W.C.
 TITLE Screening assays for agonists or antagonists of receptor activat or
 of nf-kb
 JOURNAL Patent: WO 0224896-A 5 28-MAR-2002;
 IMMUNEX CORPORATION (US)
 FEATURES
 source
 1. 954
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..954
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD37794.1"

/db_xref="GI:21698736"
 /translation="MRRASRDYTKYLRGSEMGGPGAPHEGLHAPPAPHPAPPA
 SSMFVALLIGIGVQVCSVALFFEPRAQMDPNRISDGTCHICIRILRLHFNADPDT
 TLESODTKLIPDSCKRIKQAFQCAVOKELQIIVSOHRAEKAMVDGMDLAKRSKL
 EADPFAHLITNADIPSGSHKVSLSWYHGRMAKISNMFTSNGKLIYNQDGYLYLA
 NICFRHETSGDLATEYLQIMVYVTKTSIKIPSSHTLMKGGSTRYWNSSEHFYSIN
 VGGFRLRSGEISIEVSNPSLDDPDQDARYFGAFKVRDID"

BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 46.4%; Score 121.2; DB 6; Length 954;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCGTCGACGCTCAGCCTCATCTGTTATTAATCATCATATCCCATGAG 63
 Db 473 GCAAGCTTGAAGCTCAGCTTTGCTCATCTCATCTATTATGCGCAGCATCCCATCTCG 532

QY 64 GCT--CATAAACGAGTCTTCTCTTGGAACATGACCAAGATTGGCGCAACGTCCTCA 121
 Db 533 GTTCCCATTAAGTAGTGTGCTGCTCATCTCATCTATTATGCGCAGCATCCCATCTCG 532

QY 122 ACATGACTTTCAGCAAGCAAACTAGAGTCA-----AAGGCATTATTACCGGAATG 175
 Db 593 ACATGACTTTCAGCAAGCAAACTAGAGTCA-----AAGGCATTATTACCGGAATG 652

QY 176 CCGACATTTGCTCGACATCGGCTTAACCTGAGGCTTACCTGCGAGACCTTCAGC 235
 Db 653 CCAACATTGCTTTCGACATCGGCTTAACCTGAGGACCTTACCTGAGATCTTCAAC 712

QY 236 TA 237
 Db 713 TA 714

RESULT 12
 AB064270 972 bp mRNA linear PRI 26-DEC-2001
 LOCUS AB064270
 DEFINITION Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear
 factor kappa B ligand 2-2, complete cds.
 ACCESSION AB064270
 VERSION AB064270.1 GI:18143620
 KEYWORDS
 SOURCE Homo sapiens cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Ikeda, T., Kuroyama, H. and Hirokawa, K.
 TITLE Determination of human RANKL isoforms
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 972)
 AUTHORS Ikeda, T. and Kuroyama, H.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
 University, Department of Pathology and Immunology, Graduate
 School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
 (E-mail: tohru.ph2@med.tmd.ac.jp, Tel: 81-3-5803-5176,
 Fax: 81-3-5803-0123)

FEATURES
 source
 1..972
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..972
 /gene="hRANKL 2-2"
 160..972
 /gene="hRANKL 2-2"
 /codon_start=1
 /product="receptor activator of nuclear factor kappa B
 ligand 2-2"
 /protein_id="BAB79695.1"
 /db_xref="GI:18143621"
 /translation="MFVALLIGIGVQVCSVALFFEPRAQMDPNRISDGTCHICIRIL

RLHFNADPQDTTLESQDTKLIPDSCKRIKAFQAVOKELQHVSGHTRAEKAMVDS
 SWLDAKRSKLEACPFAH/ITINATDIPSGSHKVSLSWYHRCMAKISNMTFSGNKL
 VNODGFYLYANICFRHHHTSGDLATEYLOLWVYTKTSIKIPSSHTLKKSGSTXKWS
 GNSERHFEINVGFEFKLRSGSEISIEVSNPSLDPDDQATYFGARKVDID"

BASE COUNT 270 a 219 c 249 g 234 t

ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 972;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACCTCAGCCTTCACTCATCTGTTATTAATACCATATATCCATGAG 63
 DB 491 GCAACCTTGAACCTCAGCCTTTTGGTCATCTCATCTATTAATGACACCATCCATCTG 550
 QY 64 GCT--CATAAACAGAGCTCTTCTCTTGGAAACATGACAGATTTGGGCAAGCTGCCA 121
 DB 551 GTTCCCATTAAGTGAAGTGTCTCTCTTGGTACCATGATGGGGTTGGCCAGATCTCCA 610
 QY 122 ACATGACTTTGACGACGAAAGAACTAAGATCA-----AAGCATTTATTAACCGAATG 175
 DB 611 ACATGACTTTTATGACGAAAGAACTAAGATCAAGATGGCTTTTATTAATCTGATG 670
 QY 176 CCGACATTTGCTCTGACATCGCGTAACTCAGACGCGCTAACTTCGACGAGACCTTCAGC 235
 DB 671 CCAACATTTGCTTTCGACATCATGAACCTTCAGAGACCTAGCTACAGATATCTTCAAC 730
 QY 236 TA 237
 DB 731 TA 732

RESULT 13

AB064269

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

/translation="MRRASHDYTKYLNGSEMGGPGAPHEGLHAPPHPHOPPA
 SSMFVALLGLIGVVCVSALEFVEPRAQMDPNRISDEGTHCIYRLIRLHENDFODT
 TLESODTKLIPDSCKRIKOFQAVOKELQIYSGOIRAEKAMVDGSMIDLAKRSKL
 EAOPFAHLITNATDIPSGSHKYSLSWYHNRGMAKISNMTEFSGKLIVNDGFYLYA
 NICFRHETSGDLATIEYLOLMYVYTKISIKIPSSHLMKGSGTKYWSGNSSEHFYSIN
 VGGFRLRSGEELISIEVSNPSLDPDQDATYFQAFKVRDID"

BASE COUNT 658 a 429 c 497 g 617 t
 ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 2201;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCTGACGCTCAACCTGATCTGTTATTAATCAATATCCCATGAG 63
 DB 601 GCAAGCTTGAAGCTCAGCCCTTTGCTCATCTCATATTAATGCCAGCATCCCATCTG 660
 QY 64 GCT--CATAAACGAGCTCTTCTCTTGGAACAATGACCAAGATTGGCCAAAGCTCTCA 121
 DB 661 GTTCCCATTAAGTAGAGCTGCTCTGTTGATCATGATCGGGGTTGGGCCAAAGATCTCA 720
 QY 122 ACATGACTTTCAGCAGCAAGAACTAAGAGTCA-----AAGCATTTATTAACCGAATG 175
 DB 721 ACATGACTTTCAGCAGCAAGAACTAAGTAAATCAGAGATGGCTTTATTAATCTGTATG 780
 QY 176 CCGACATTTGCTCTCGACATCGGTAACCTCAGAGGCTTAACCTGAGGACCTTCAGC 235
 DB 781 CCAACATTTGCTCTTCGACATCATGAACCTTCAGGAGACCTTAACAGATATCTTCAAC 840
 QY 236 TA 237
 DB 841 TA 842

RESULT 15
 AF053712 2271 bp mRNA linear PRI 09-MAY-1998
 LOCUS Homo sapiens osteoprotegerin ligand mRNA, complete cds.
 DEFINITION AF053712
 ACCESSION AF053712.1 GI:3057145
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 2271)
 Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
 Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
 Hew, H., Sullivan, J., Hawkins, N., Davy, E., Caparrelli, C., Eli, A.,
 Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
 Delaney, J. and Boyle, W.J.

Osteoprotegerin ligand is a cytokine that regulates osteoclast
 differentiation and activation

JOURNAL Cell 93 (2), 165-176 (1998)
 MEDLINE 98227661
 PUBMED 9568710

REFERENCE 2 (bases 1 to 2271)
 Boyle, W.J.

Direct Submission
 Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
 One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES
 SOURCE
 1. 2271
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 185. .1138
 /function="regulates osteoclast differentiation and
 activation"

CDS

/codon_start=1
 /product="osteoprotegerin ligand"
 /protein_id="AAC39731.1"
 /db_xref="GI:3057146"
 /translation="MRRASHDYTKYLNGSEMGGPGAPHEGLHAPPHPHOPPA

SSMFVALLGLIGVVCVSALEFVEPRAQMDPNRISDEGTHCIYRLIRLHENDFODT
 TLESODTKLIPDSCKRIKOFQAVOKELQIYSGOIRAEKAMVDGSMIDLAKRSKL
 EAOPFAHLITNATDIPSGSHKYSLSWYHNRGMAKISNMTEFSGKLIVNDGFYLYA
 NICFRHETSGDLATIEYLOLMYVYTKISIKIPSSHLMKGSGTKYWSGNSSEHFYSIN
 VGGFRLRSGEELISIEVSNPSLDPDQDATYFQAFKVRDID"

BASE COUNT 658 a 462 c 522 g 629 t
 ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 2271;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCTGACGCTCAACCTGATCTGTTATTAATCAATATCCCATGAG 63
 DB 657 GCAAGCTTGAAGCTCAGCCCTTTGCTCATCTCATATTAATGCCAGCATCCCATCTG 716
 QY 64 GCT--CATAAACGAGCTCTTCTCTTGGAACAATGACCAAGATTGGCCAAAGCTCTCA 121
 DB 717 GTTCCCATTAAGTAGAGCTGCTCTGTTGATCATGATCGGGGTTGGGCCAAAGATCTCA 776
 QY 122 ACATGACTTTCAGCAGCAAGAACTAAGAGTCA-----AAGCATTTATTAACCGAATG 175
 DB 777 ACATGACTTTCAGCAGCAAGAACTAAGTAAATCAGAGATGGCTTTATTAATCTGTATG 836
 QY 176 CCGACATTTGCTCTCGACATCGGTAACCTCAGAGGCTTAACCTGAGGACCTTCAGC 235
 DB 837 CCAACATTTGCTCTTCGACATCATGAACCTTCAGGAGACCTTAACAGATATCTTCAAC 896
 QY 236 TA 237
 DB 897 TA 898

Search completed: December 8, 2002, 18:32:01
 Job time : 678.919 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:16:58 ; Search time 2565.48 Seconds
(without alignments)
7329.213 Million cell updates/sec

Title: us-09-880-457-1

Sequence: 1 aaaagaggaataatcaagaa.....taataaaggaggaataatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estda:*
2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95.8	8.3	659	AG107545	AG107545 Pan trogl
2	84.8	7.3	612	BH267783	BH267783 CH230-186
3	75.8	6.5	362	AV653073	AV653073 AV653073
4	48	4.1	598	BF724774	BF724774 bx08e07.y
5	46.4	4.0	487	B92778	B92778 CTT-HSP-216
6	44	3.8	372	AA337226	AA337226 EST42291

7	44	3.8	550	10	AW966229	EST378302
C	9	43.8	407	17	AO085343	HS_2164_B
C	8	43.6	855	17	CNS011PE	AL100556 Drosophila
C	10	43.4	198	17	BG197160	RST16397
C	11	43.4	438	17	AO669724	HS_3581_A
C	12	43.2	355	17	AO013160	AO013160 CTT-HSP-2
C	13	42.4	384	13	BG940945	ax08d07.x
C	14	42.2	626	17	AG154770	Pan trogl
C	15	41.8	276	12	BG203357	RST22738
C	16	41.8	299	12	BG206497	RST25946
C	17	41.8	892	17	CNS03PER	AL241625 Tetradon
C	18	41.8	975	17	CNS02KBD	AL201298 Tetradon
C	19	41.8	979	17	B18713	B18713 F28L3-17 IG
C	20	41.6	502	17	AO142682	HS_2222_B
C	21	41.4	615	17	AO538505	RPCI-11-3
C	22	40.6	444	9	A1223309	q971a07.x
C	23	40.6	645	9	A1286243	q102909.x
C	24	40.4	645	17	B19590	T29F5-17.3
C	25	40.2	645	17	B19590	T29F5-17.3
C	26	40.2	277	12	BG184205	RST3126_A
C	27	40	679	17	AG154560	Pan trogl
C	28	40	773	17	AO743573	HS_5385_B
C	29	39.6	414	9	AA814937	oc07c12.s
C	30	39.6	641	10	BE081027	QV1-BT063
C	31	39.6	690	17	AO490150	RPCI-11-2
C	32	39.6	997	17	CNS005TE	AL060767 Drosophila
C	33	39.6	1027	14	B0050697	AGENCOURT
C	34	39.2	404	10	AW975966	EST388075
C	35	39.2	412	9	A1201905	q142e03.x
C	36	39.2	644	10	AW749542	QV4-BT040
C	37	39.2	680	14	BQ182337	UI-H-BU0
C	38	39.2	714	17	AG173653	Pan trogl
C	39	39.2	733	13	BM666955	UI-E-C11-
C	40	39.2	3405	11	BC026895	Homo sapi
C	41	39	331	11	BG382085	297855_MA
C	42	39	428	10	AW027590	w65B05.x
C	43	39	623	17	AO021146	AO021146 CTT-HSP-2
C	44	38.8	269	14	F03748	HSC28F022 n
C	45	38.8	472	17	AO580608	RPCI-11-4

ALIGNMENTS

RESULT 1
LOCUS AG107545 659 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
ACCESSION AG107545
VERSION AG107545.1 GI:16728063
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB Unpublished
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenho-cho, Tsukuba, Ibaraki, Japan, Kanagawa 230-0045, Japan (E-mail:chimpanzee@riken.go.jp, URL:http://hsp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Rad process and may have higher chance of clone tracking errors.

	PRIMERS
	Sequencing: -21M13
	LIBRARY
	Vector : PKS145
	R.Site 1 : SacI
	R.Site 2 : SacI.
	Location/Qualifiers
	1..659
	/organism="Pan troglodytes"
	/db_xref="taxon:9598"
	/clone="PTB-112G09.F"
	/sex="male"
	/cell_type="Lymphoblast"
	/clone_idb="PTB Chimpanzee Male BAC Library"
BASE COUNT	181 a 168 c 121 g 189 t
ORIGIN	
Query Match	8.3%; Score 95.8; DB 17; Length 659;
Best Local Similarity	71.1%; Pred. No. 1,6e-16;
Matches 143; Conservative	0; Mismatches 52; Indels 6; Gaps 1
OY	528 ATACATCAATPCCCATAGAGGCTCATAAAGACAGCTTCTCTTGGAACATGACCAA 567
Dd	
Dd	388 ATGCCTCTTTCTCCACAGGTTCCTAAGAATGATGTCCTCGTAGCACATGATCG 447
OY	586 GATTGGGCAACGCTCTCCAACATGACTTTCAGACAAGAAAATAAGATCA-----AA 641
Dd	
OY	448 GTTGTGGCCCAATGCTCCAACATGACTTTAGCAATGAAACTATATGTTATACGAT 507
OY	642 GGCAATTTATACCGAATGCCGACATTTCTCTGCATTCGGTAACCTGACGAGCCTTA 701
Dd	
OY	508 GCCTTTATACCTGATGATCCCAACATTTGCTTTCGACATCATGAAACTTCAGAGACCTTA 567
Dd	
OY	702 ACTCTGACGAGACCTTCAGCTA 722
Dd	
Dd	568 CCTACAGATATCTTCACCTA 588
RESULT 2	
BH267783/c	
LOCUS	BH267783 .612 bp DNA linear GSS 30-NOV-2001
DEFINITION	CH230-186c1.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION	CH230-186c1, DNA sequence.
VERSION	BH267783
KEYWORDS	BH267783.1 GI:17180093
SOURCE	GSS.
ORGANISM	Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 612)
AUTHORS	Zhao,S., Shelly,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn, A., Gebregregoris,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999) Other-GSSs: CH230-186c1.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhaoe@tigr.org
TITLE	Clones are derived from the rat BAC library CHORI-230
JOURNAL	(http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org).
COMMENT	Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or_eirng_information.htm). BAC end page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html Plate: 186 row: c column: 1 Seq primer: T7

Class: BAC ends.
Location/Qualifiers
1..612

/organism="Rattus norvegicus"
/strain="BN/SnHsd/MCw"
/db_xref="taxon:10116"
/clone="CH230-186c1"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
Pleter de Jong"

BASE COUNT 168 a 145 c 133 g 166 t

ORIGIN

Query Match 7.3%; Score 84.8; DB 17; Length 612;
Best Local Similarity 69.5%; Pred. No. 2.4e-13;
Matches 132; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 538 TATCCCATGAGGCTCAATAAACAAGACTCTTCCTTGTAAGAAGTACCAAGATTGGCAA 597
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 603 TCCTCTAGGTGCCATTAAGTCAGTCTGTCTTCCTTGTAACCATGATCGAGGCTGGCCA 544
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 598 ACCTCTCCAACTGACTTTGCAGCAACGAAAACCTAACGTC-----AAGCATTTATT 651
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 543 AGATCTCTAACATGACGTTTAGCAACGAAAACTAAGGTTTAACCAGATGCTCTATT 484
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 652 ACCGAATCCGCAGATTCTCTCGCATCGCGGTAACTCACAGGCGCTTAAGTTCGAG 711
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 483 ACGTGTAGCCCAACATTCTCTTCAGGCATCATGAACTCAAGGAGCGTAACTCGCGACT 424
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 712 ACCTCAGCT 721
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 423 ATCTTCAGCT 414
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
AV653073 362 bp mRNA linear EST 15-JAN-2002

LOCUS
DEFINITION AV653073 GLC Homo sapiens cdna clone GLCDHB01 3', mRNA sequence.

ACCESSION AV653073

VERSION AV653073.1 GI:9874087

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 362)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Ou,J., Liu,F., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z., and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE

JOURNAL MEDLINE

COMMENT
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCDHB01"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"

FEATURES
SOURCE

```

/dev.stage="Adult"
/lab.host="SOLR"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      102 a      80 c      78 g      100 t      2 others
ORIGIN
Query Match      6.5%; Score 75.8; DB 10; Length 362;
Best Local Similarity 71.5%; Pred. No. 8.2e-11;
Matches 113; Conservative 0; Mismatches 43; Indels 2; Gaps 1;

QY 465 CAGGAGAGATTGCTTAAGATGCAATCCCTGACGCTCAACATCTTGTGA 524
      || || || || || || || || || || || || || || || || ||
DB 204 CAGGTGTAAGTCTGCGCAAGAGAGCAAGCTGAGCTTCAGCTCATCTCACTA 263
      || || || || || || || || || || || || || || || || ||
QY 525 TTAATACCATCATATATCCCATGAGCT--CATAAACGAGCTTTCTTCTTGGAACATG 582
      || || || || || || || || || || || || || || || || ||
DB 264 TTAATGCCACCGACATCCCATCTGTTCCCATAAAGTGTCTGCTTGTGATACCATG 323
      || || || || || || || || || || || || || || || || ||
QY 583 ACCAAGATGGGCAACGCTCTCCAACTGACTTCAGC 620
      || || || || || || || || || || || || || || || || ||
DB 324 ATCGGCTGTGGCCAGATCTCAACATGACTTTAGC 361
      || || || || || || || || || || || || || || || || ||

RESULT 4
BF724774/c 598 bp mRNA linear EST 05-JAN-2001
LOCUS      bx08e07.y1 Human Iris cDNA (un-normalized, unamplified): BX Homo
DEFINITION sapiens cDNA clone bx08e07 5', mRNA sequence.
ACCESSION  BF724774
VERSION     BF724774.1 GI:12040685
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 598)
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES      Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
JOURNAL     NEIBANK: EST analysis and bioinformatics for ocular genomics
COMMENT     Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: giraemehelix.nih.gov
            Plate: 08 row: e column: 07
            Seq primer: M13RPI reverse primer (ABI).
FEATURES
SOURCE      Location/Qualifiers
            1..598
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="bx08e07"
            /clone_lib="Human Iris cDNA (un-normalized, unamplified):
            BX"
            /tissue.type="Iris"
            /dev.stage="Adult"
            /lab.host="EMDH10B"
            /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
            tissue was pooled from 10 individuals ranging in age from
            4-80 years and RNA was extracted. From this pooled sample
            an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
            directionally cloned cDNA library in the pCMVSPORT6 vector
            was constructed at Life Technologies, essentially
            following the protocols of the Superscript Plasmid System
            full details of which are contained in the manufacturer's
            instruction manual (http://www.lifetech.com/). First
            strand synthesis was carried out using a Not I
            primer-adapter [5'-pgactagttctatgacgcgacgccc(7)15-3'
            ]. Not I blunt end inserts were cloned into the Not I/EcoR
            v sites in the vector. EST analysis was performed on the
            unamplified library at the NIH Intramural Sequencing

```

```

Center (NISC)."
BASE COUNT      161 a      142 c      146 g      149 t
ORIGIN
Query Match      4.1%; Score 48; DB 12; Length 598;
Best Local Similarity 68.8%; Pred. No. 0.011;
Matches 66; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 348 AGTATCTACAGGACGACGATTTTGTGACATTTGGGATTTGACCAACAAGTCAG 407
      || || || || || || || || || || || || || || || || ||
DB 96 AGTGTCTACTGTGACAGGATGTTGTTACGGCTGGGATATGACATTAACAAGCAG 37
      || || || || || || || || || || || || || || || || ||
QY 408 ACAAAAACCTTGCTCTGTTGAGGAGGAACATTTAG 443
      || || || || || || || || || || || || || || || || ||
DB 36 GCAAAAATCCTGACCTCATGAACTGACCTTTAG 1
      || || || || || || || || || || || || || || || || ||

RESULT 5
B92778      487 bp DNA linear GSS 25-JUN-1998
LOCUS      CIT-HSP-2164D13.TR CIT-HSP Homo sapiens genomic clone 2164D13, DNA
DEFINITION sequence.
ACCESSION  B92778
VERSION     B92778.1 GI:2975115
KEYWORDS   GSS.
SOURCE      human.
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 487)
AUTHORS     Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLES      Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
JOURNAL     Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
COMMENT     Simon,M. and Venter,J.C.
            Use of a random BAC End Sequence Database for Sequence-Ready Map
            Building (1998)
            Unpublished (1998)
            Other_GSSs: CIT-HSP-2164D13.TF
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (Info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES
SOURCE      Location/Qualifiers
            1..487
            /organism="Homo sapiens"
            /db_xref="GDB:7100687"
            /db_xref="taxon:9606"
            /clone="2164D13"
            /clone_lib="CIT-HSP"
            /sex="Male"
            /cell.type="Sperm"
            /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
            HindIII"
BASE COUNT      147 a      104 c      83 g      152 t      1 others
ORIGIN
Query Match      4.0%; Score 46.4; DB 17; Length 487;
Best Local Similarity 60.2%; Pred. No. 0.03;
Matches 77; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 349 GTATCTACAGGACGACGATTTTGTGACATTTGGGATTTGCGCAACAAGTCAGA 408
      || || || || || || || || || || || || || || || || ||
DB 182 GTGCCCACTATGACCAAGCAATGATATCTGAAATTCAGCAAGCAAGACAGA 123
      || || || || || || || || || || || || || || || || ||
QY 409 CAAAAAACCTTGCTGTGGTGGAGGAACATTTAGCAAAAGGAGCAATAGCAAGCAGG 468
      || || || || || || || || || || || || || || || || ||

```

Db 122 CAAACACCCCTGCTGTCAGCTTCTATCATTTGACCTCCAGGAGACAGAAAGAA 63
 OY 469 AGAGCTAT 476
 Db 62 TGATATTT 55

RESULT 6
 AA337226 372 bp mRNA linear EST 21-APR-1997
 LOCUS EST42291 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.
 DEFINITION AA337226
 ACCESSION AA337226 GI:1989784
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 372)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,
 C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
 O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clayton,R.A.,
 Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fine,L.D., Fitzgerald,
 L.M., Fitzhugh,W.M., Fitchman,U.L., Geoghegan,N.S., Glodex,A.,
 Gheum,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
 Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dunke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.M.,
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
 Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L.,
 Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
 M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
 Venter,J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 JOURNAL based upon 83 million nucleotides of cDNA sequence
 MEDLINE Nature 377 (6547 Suppl.), 3-174 (1995)
 COMMENT 96026280
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..372
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):139297"
 /db_xref="taxon:9606"
 /clone_lib="Endometrial tumor"
 /sex="female"
 /dev_stage="adult"
 /note="Organ: endometrium; Vector: pBluescript SK-;
 Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 106 a 78 c 104 g 83 t 1 others
 ORIGIN

Query Match 3.8%; Score 44; DB 9; Length 372;
 Best Local Similarity 70.2%; Pred. No. 0.13; Mismatches 25; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 368 CATTTTTCAGCATTTGGATTTGTGACAAAGTCAGACAAAACCTGCTGTGT 427
 Db 90 CTTGTTCAGGACCTTGATTCACCATATACATGAGACAAAATCCCTGCCCTGGA 149
 OY 428 GGAGGACATCTCTACCAAGGAA 451

Db 150 GACGCTTACATTTCTAGCATGGCAA 173

RESULT 7
 AM966229 550 bp mRNA linear EST 01-JUN-2000
 LOCUS AM966229
 DEFINITION EST378302 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM966229
 VERSION AM966229.1 GI:8156065
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 550)
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspari,R., Gay,C., Holt
 T.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeaman,T.J. and
 Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor
 JOURNAL metastasis using a 19,200 element cDNA microarray
 COMMENT Unpublished (2000)
 Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 224
 Seq primer: Reverse.
 Location/Qualifiers
 1..550
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGI"
 /note="Vector: pBluescriptSKm"
 BASE COUNT 165 a 107 c 146 g 132 t
 ORIGIN

Query Match 3.8%; Score 44; DB 10; Length 550;
 Best Local Similarity 70.2%; Pred. No. 0.15; Mismatches 25; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 368 CATTTTTCAGCATTTGGATTTGTGACAAAGTCAGACAAAACCTGCTGTGT 427
 Db 89 CTTGTTCAGGACCTTGATTCACCATATACATGAGACAAAATCCCTGCCCTGGA 148
 OY 428 GGAGGACATCTCTACCAAGGAA 451
 Db 149 GACGCTTACATTTCTAGCATGGCAA 172

RESULT 8
 AO085343/C 407 bp DNA linear GSS 26-AUG-1998
 LOCUS AO085343
 DEFINITION HS_2164_B1_B07_MR CTR Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate-2164 Col-13 Row-D, DNA sequence.
 ACCESSION AO085343
 VERSION AO085343.1 GI:3454560
 KEYWORDS
 SOURCE GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 407)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 JOURNAL scanning the human genome
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 COMMENT 99380589
 Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Sequence Tagged Connector
Plate: 2164 row: D column: 13
Class: BAC ends
High quality sequence stop: 407.
Location/Qualifiers

FEATURES

source

1..407
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2164 Col=13 Row=D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT

120 a 82 c 75 g 129 t 1 others

ORIGIN

Query Match 3.8%; Score 43.8; DB 17; Length 407;
Best Local Similarity 60.5%; Pred. No. 0.16; Mismatches 0; Gaps 0;
Matches 72; Conservative 0; Indels 47; Indels 0;

QY 349 GTATCTACAGGACACGATTTTGTGAGATTTGTCAGCAACAGTCAGA 408

Db 126 GTGCCACTATGACACGACATGATATGATTCAGATTCAGACACAGACAGA 67

QY 409 CAAAAAAGCTTCTGTGTGAGGACATTCAGCAAGAGCAATGACAGACAG 467

Db 66 CAAAAACACCCGCGTGTCAAGCTTATCATTCACCTCCAGGAGACAGAAAG 8

RESULT 9

CNS011PE

LOCUS

DEFINITION 855 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN06M20 of DrosBAC library from Drosophila melanogaster (fruit
fly) genomic survey sequence.

ACCESSION AL100556

VERSION AL100556.1 GI:5612167

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster.

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

AUTHORS

Ephyrtoidea; Drosophilidae; Drosophila.

TITLE

1 (bases 1 to 855)

JOURNAL

Genoscope.

COMMENT

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

REFERENCE

BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr

AUTHORS

- Web : www.genoscope.cns.fr)

TITLE

determination of this BAC-end sequence was carried out as part of a

JOURNAL

collaboration with the European Drosophila Genome Project (EDGP) -

FEATURES

http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC

source

library (DrosBAC) was made by Alain Billard at CEPH (Centre

BASE COUNT

d'Etude du Polymorphisme Humain) with funding provided by a MRC

ORIGIN

and geneieve Payan. It has been constructed in the vector

1..855

Location/Qualifiers

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACN06M20"

/clone_lib="DrosBAC"

/plasmid="pBelobAC11"

/note="end : SP6"

Query Match 3.8%; Score 43.6; DB 17; Length 855;
Best Local Similarity 11.5%; Pred. No. 0.23;
Matches 64; Conservative 148; Mismatches 346; Indels 0; Gaps 0;

QY 393 CAGCAACAAAGTCAGACAAAAACCTTGTCTGTGAGGAGACATTTAGCAAGAG 452

Db 250 MAM 309

QY 453 GCAATGACAGGAGGAGGATTTGCTAGATTCGCAATCCGACCTCAGCCTTCA 512

Db 310 NNNMAM 369

QY 513 CTGATCTTTGATTAATACATCAATATCCATGAGGCTCAATAACGAGCTTCTTCT 572

Db 370 MTMTNTNTNTMTCTNTCCMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 429

QY 573 TCGAATCATGACCAAGATTTGGGCAACGCTTCACATGACTTTCAGCAAGGAAACTA 632

Db 430 NNN 489

QY 633 AGAGTCAAGGCAATTTATCCGGAATGCCGACATTTGCTTCGACATCGGTAACCTCA 692

Db 490 MMTNTMT 549

QY 693 CGAGGCTTAATCTGACGACCTTCAGCTATGATGATTAATGAGATCATTCACAGACA 752

Db 550 GNTTNN 609

QY 753 TCAACTATGTACACGATTTGGGTGGTGCAGAGATCAAGACTTAAGACCAAAACC 812

Db 610 TTTTNN 669

QY 813 TGCCTCCAGGAAG 872

Db 670 MAM 729

QY 873 CCGTAGAGGAGGAGGAGTGGTGTGCTGAGGAGACCAAGAGATTAATGCGGGAGAGC 932

Db 730 KMSGGMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAM 789

QY 933 CCGGGAAGAGATGAGATT 950

Db 790 KTGKMTMTMTMTMTMTMT 807

RESULT 10

Bg197160/c

LOCUS

Bg197160 198 bp mRNA linear EST 21-APR-2001

DEFINITION

RST16397 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION

Bg197160

VERSION

Bg197160.1 GI:13718847

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE

1 (bases 1 to 198)

JOURNAL

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,

MEDLINE

Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,

COMMENT

Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave,

Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@athersys.com

High quality sequence stop: 148.

FEATURES

SOURCE

Location/Qualifiers
1..198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="H1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT

55 a 56 c 41 g 46 t

ORIGIN

Query Match 3.7%; Score 43.4; DB 12; Length 198;
Best Local Similarity 69.4%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 465 CAGGAGAGTATTGCTAGATGCAATGCGAGCGCTGAGCTTCACTCATCTTGT 524

DB 140 CATGCTTAGATCTGGCCAGAGGAGCAAGCTTGAAGCTTGTGCTCATCTACTA 81

OY 525 TTATATACCATCATATCCCATGAGG 549

DB 80 TTAATGCCACGACATCCCATGTGG 56

RESULT 11

LOCUS

A0669724 438 bp DNA linear GSS 24-JUN-1999
HS_5381_A1_P01_SP6E_RPCI-11 Human Male BAC Library Homo sapiens

ACCESSION A0669724 GI:5202558

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 438)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 957 row: K column: 1
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 438.

FEATURES

SOURCE

Location/Qualifiers
1..438
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="957 Col=1 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"
pBACE3.6 vector at EcoRI sites
1 others

BASE COUNT

166 a 87 c 62 g 122 t

ORIGIN

Query Match 3.7%; Score 43.4; DB 17; Length 438;
Best Local Similarity 69.4%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY

363 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGCT 422

DB

104 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGCT 163

OY

423 CTGTGGAGGGAGCATTTCTAGCAAA 447

DB

164 TTTGTGAGAGCTTACATTTCTAAATA 188

RESULT 12

LOCUS

A0013160 355 bp DNA linear GSS 06-JUN-1998
CIT-HSP-2298M3.TF CIT-HSP Homo sapiens genomic clone 2298M3, DNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 355)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mhadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

SOURCE

Location/Qualifiers
1..355
/organism="Homo sapiens"
/db_xref="GDB:715385"
/db_xref="taxon:9606"
/clone_plate="2298M3"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT

113 a 67 c 83 g 92 t

ORIGIN

Query Match 3.7%; Score 43.2; DB 17; Length 355;
Best Local Similarity 60.0%; Pred. No. 0.22; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY

363 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGCT 422

DB

163 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGCT 222

LOCUS	276 bp	mRNA	linear	EST 21-APR-2001
DEFINITION	BC203357	Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BC203357			
VERSION	BC203357.1	GI:13725044		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 276)			
AUTHORS	Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Jenner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,J., Veloso,N., Kilka,A., Hess,J., Cothen,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.			
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression			
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)			
MEDLINE	21227151			
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@atersys.com			
FEATURES	High quality sequence stop: 276. location/Qualifiers			
SOURCE	1. 276 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."			
BASE COUNT	92 a 51 c 59 g 74 t			
ORIGIN				
Query Match	3.6%; Score 41.8; DB 12; Length 276;			
Best Local Similarity	68.2%; Pred. No. 0.52;			
Matches	58; Conservative % 0; Mismatches 27; Indels 0; Gaps 0;			
QY	465 CAGGAGAGTATTTCGTAGACATGGCAATCTCTGACGCTGACCCCTTCAACATCATCTTGTTA 524			
Db	91 CATGGTTAGATCTGCGCCAGAGAGCAAGCTTGAAGCTCACCTTTGTCATCTCACTA 32			
OY	525 TTAAATACATCAATATATCCCATGAGG 549			
Db	31 TTAAATGCCACCGACATCTGG 7			

GenCore version 5.1.3
(c) 1993 - 2002 Compu

pleic search, using sw model

December 8, 2002, 15:56:14 ; Search time 330.592 Seconds
(without alignments)
7908.746 Million cell updates/

US-09-880-457-1

1 aaagagygataattcaagaa.....taataaaggygaaatgc 1161

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

2185239 seqs, 1125999159 residues

hits satisfying chosen parameters: 4370478

```
length: 0
length: 2000000000000
```

Maximum Match	100%
Minimum Match	0%

Listing first 45 summaries

N_Geneseq_101002:*

1:	/SID2/gcgdata/genseq/genseqn-emb1/NA1980.DAT *
2:	/SID2/gcgdata/genseq/genseqn-emb1/NA1981.DAT *
3:	/SID2/gcgdata/genseq/genseqn-emb1/NA1982.DAT *
4:	/SID2/gcgdata/genseq/genseqn-emb1/NA1983.DAT *
5:	/SID2/gcgdata/genseq/genseqn-emb1/NA1984.DAT *
6:	/SID2/gcgdata/genseq/genseqn-emb1/NA1985.DAT *
7:	/SID2/gcgdata/genseq/genseqn-emb1/NA1986.DAT *
8:	/SID2/gcgdata/genseq/genseqn-emb1/NA1987.DAT *
9:	/SID2/gcgdata/genseq/genseqn-emb1/NA1988.DAT *
10:	/SID2/gcgdata/genseq/genseqn-emb1/NA1989.DAT *
11:	/SID2/gcgdata/genseq/genseqn-emb1/NA1990.DAT *
12:	/SID2/gcgdata/genseq/genseqn-emb1/NA1991.DAT *
13:	/SID2/gcgdata/genseq/genseqn-emb1/NA1992.DAT *
14:	/SID2/gcgdata/genseq/genseqn-emb1/NA1993.DAT *
15:	/SID2/gcgdata/genseq/genseqn-emb1/NA1994.DAT *
16:	/SID2/gcgdata/genseq/genseqn-emb1/NA1995.DAT *
17:	/SID2/gcgdata/genseq/genseqn-emb1/NA1996.DAT *
18:	/SID2/gcgdata/genseq/genseqn-emb1/NA1997.DAT *
19:	/SID2/gcgdata/genseq/genseqn-emb1/NA1998.DAT *
20:	/SID2/gcgdata/genseq/genseqn-emb1/NA1999.DAT *
21:	/SID2/gcgdata/genseq/genseqn-emb1/NA2000.DAT *
22:	/SID2/gcgdata/genseq/genseqn-emb1/NA2001A.DAT *
23:	/SID2/gcgdata/genseq/genseqn-emb1/NA2001B.DAT *
24:	/SID2/gcgdata/genseq/genseqn-emb1/NA2002.DAT *

is the number of results predicted by chance to have a greater than or equal to the score of the result being printed derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	268	23.1	1186	24	AAK33576	CDNA encoding huma
2	126.2	10.9	741	19	AAV69899	Nucleic acid encoco
3	126	10.9	954	19	AAV69887	Nucleic acid encoco
4	126	10.9	954	19	AAV41378	NF-KB receptor acti
5	126	10.9	954	19	AAV41372	NF-KB receptor acti
6	126	10.9	954	22	AAD15311	Human receptor acti
7	126	10.9	954	22	AAD08715	Human receptor acti
8	126	10.9	954	22	AAD05604	Human full-length
9	126	10.9	1945	24	ABK12877	CDNA encoding huma

10	126	10.9	2226	24	ABK12876	cDNA encoding human
11	126	10.9	2271	21	AAZ999664	DNA encoding a hum
12	126	10.9	2374	19	AAV70285	Human osteoprotege
13	126	10.9	2390	24	ABK40274	cDNA encoding huma
14	122.8	10.6	1823	20	AAK80223	Human TRANCE encod
15	102	8.8	957	22	AAF86481	Rat osteoclast dif
16	97	8.4	735	19	AAV69898	Nucleic acid encod
17	97	8.4	951	19	AAV69900	Nucleotide sequenc
18	97	8.4	951	21	AAA39156	Mouse OBM nucleoti
19	97	8.4	951	21	AAZ99865	DNA encoding a mur
20	97	8.4	951	21	AAZ49024	Osteoclast formati
21	97	8.4	1538	19	AAV69886	Nucleic acid encod
22	97	8.4	1574	22	AAH25526	Nucleotide sequenc
23	97	8.4	1630	19	AAV41377	NF-kB receptor acti
24	97	8.4	1630	19	AAV41371	NF-kB receptor acti
25	97	8.4	1630	22	AAD15310	Murine receptor ac
26	97	8.4	1630	22	AAD08714	Murine receptor ac
27	97	8.4	1630	22	AAD05903	Murine RANKL (rece
28	97	8.4	2191	19	AAV41489	Nucleotide sequenc
29	97	8.4	2237	20	AAK80224	Murine TRANCEenco
30	97	8.4	2237	24	ABK12880	cDNA encoding mous
31	97	8.4	2295	19	AAV70284	Human osteoprotege
32	97	8.4	2299	21	AAZ99866	DNA encoding a mur
33	94.4	8.1	522	22	AAK13369	Mouse cDNA encodin
34	81.6	7.0	2029	21	AAZ93155	Mouse OBM nucleoti
35	74.2	6.4	519	21	AAZ998968	DNA encoding a syrn
36	74.2	6.4	519	21	AAZ998969	DNA encoding a muru
37	74.2	6.4	519	21	AAZ998972	DNA encoding osteo
38	74.2	6.4	564	21	AAZ998967	DNA encoding a syrn
39	73.4	6.4	564	21	AAZ998970	DNA encoding osteo
40	73.8	6.4	546	21	AAZ99971	DNA encoding osteo
41	63.2	5.0	519	21	AAZ99973	DNA encoding osteo
42	46.2	4.0	1000	21	AAH51592	Human G1C1 related
43	45	3.9	1001	21	AAH51308	Human G1C1 related
44	44	3.8	659	22	AAH00215	Human reproductive
45	44	3.8	983	22	AAH34950	Human colon cancer

ALIGNMENTS

RESULT	1
ABK33576	
ID	ABK33576 standard; cDNA, 1186 BP.
XX	
AC	ABK33576;
XX	
DJ	08-MAY-2002 (first entry)
XX	
DE	cDNA encoding human PRO protein, Seq ID No 81.
XX	
KW	Human; secreted protein; PRO; tumour; lung cancer; colon cancer
KW	breast cancer; prostate tumour; rectal tumour; liver tumour;
KW	pelvic/cell proliferation; chondrocyte cell proliferation;
XX	tumour necrosis factor-alpha; gene; ss.
OS	Homo sapiens.
XX	
PN	WO200208288-A2.
PD	
XX	
PD	31-JAN-2002.
XX	
PF	29-JUN-2001; 2001MO-US21066.
XX	
PR	20-JUL-2000; 2000US-219556P.
PR	25-JUL-2000; 2000US-220583P.
PR	25-JUL-2000; 2000US-220603P.
PR	25-JUL-2000; 2000US-220607P.
PR	25-JUL-2000; 2000US-220624P.
PR	25-JUL-2000; 2000US-220638P.
PR	25-JUL-2000; 2000US-220664P.
PR	25-JUL-2000; 2000US-220666P.
PR	26-JUL-2000; 2000US-220893P.

28-JUL-2000; 2000MO-US20710.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23528.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001MO-US17092.

(GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2002-172001/22.
 P-PSDB: AAU83632.

One hundred and twenty two nucleic acids encoding PRO polypeptides,
 useful for treating a PRO related disorder and for diagnosing tumours
 such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 tumour or liver tumour -

Claim 2: Figure 81; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK3536-ABK3567 represent human
 CC PRO protein coding sequences of the invention.

XX Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;

Query Match 23.1%; Score 268; DB 24; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 3.6e-76;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAGTATTTGCTAGAAATGCAATCTGACCTGACCTTCAACTCATTCTTTATTA 528
 Db 430 AGAGTATTTGCTAGAAATGCAATCTGACCTGACCTTCAACTCATTCTTTATTA 489
 QY 529 TACATCAATATCCATGAGGCTCAATAAAGAGTCTTCTTCTTGGAAACATGACCAAG 588
 Db 490 TACATCAATATCCATGAGGCTCAATAAAGAGTCTTCTTCTTGGAAACATGACCAAG 549
 QY 589 ATTGGGCAAGAGTCTCCCAATGACTTTCAGCAAGGAAACTAGAGTCAAAAGCATTT 648
 Db 550 ATTGGGCAAGAGTCTCCCAATGACTTTCAGCAAGGAAACTAGAGTCAAAAGCATTT 609
 QY 649 ATTACCGGAATGCGAGCAATTTGCTCGACATCGGTACCTCAGAGGCGTAACTCTGC 708
 Db 610 ATTACCGGAATGCGAGCAATTTGCTCGACATCGGTACCTCAGAGGCGTAACTCTGC 669
 QY 709 AGGACTTCACTATGATGTAATTTGAG 736
 Db 670 AGGACTTCACTATGATGTAATTTGAG 697

RESULT 2

AAV69899
 ID AAV69899 standard; cDNA to mRNA; 741 BP.

XX AAV69899;

XX 10-FEB-1999 (first entry)

XX Nucleic acid encoding a human OCIF-binding molecule (OBM).

XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT 1..741
 FT CDS /*tag= a

XX WO9846644-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-JP01728.

XX 02-DEC-1997; 97JP-0332241.

XX 15-APR-1997; 97JP-0097808.

XX 09-JUN-1997; 97JP-0151434.

XX 12-AUG-1997; 97JP-0217897.

XX 21-AUG-1997; 97JP-0224803.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PT Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX WPI: 1998-594563/50.
 P-PSDB: AAW83020.

XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism

XX Example 28; Pages 121-122; 151pp; Japanese.

XX The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a soluble form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.

XX Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;

Query Match 10.9%; Score 126.2; DB 19; Length 741;
 Best Local Similarity 68.2%; Pred. No. 3.8e-30;
 Matches 223; Conservative 0; Mismatches 93; Indels 11; Gaps 3;

QY 407 GACAAAGAACCTGCTGCTGAGGAGGAGCAATTTAGCAAGGAAGCAATGACAG-- 464
 Db 175 GAATTTACACATATCTGTTGGATCACAGCACATCAAGAGAGGAGGATGATGATGATG 234
 QY 465 -CAGAGAGAGTATTTGCTAGAAATGCAATCTGACCTGACCTTCAACTCATTCTTGT 523
 Db 465 -CAGAGAGAGTATTTGCTAGAAATGCAATCTGACCTGACCTTCAACTCATTCTTGT 523

Db 235 TCATGGTTAGATCTGGCCAGAGGAGCAAGCTTGAGCTTTTGTCTCATCTCACT 294
 Qy 524 ATTAATACATCATATATCCCATGAGCT--CATAAACGAGTCTTTCTTGTGAAACAT 581
 Db 295 ATTAATGCCACCAACATCCCATCTGTTCCCATTAAGTGAAGTCTGCTCTTGAGCAT 354
 Qy 582 GACCAAGATTTGGGCAACGCTCCACATCTTTCAGCAGCGAAACTAAGAGTCA-- 639
 Db 355 GATCGGGGTTGGGCCAAGATCTCCACATGACTTTTACCAATGGAACCTAATAGTTAAT 414
 Qy 640 ---AAGCATTTATTAACCGAATGCGGACATTTGCTCGACATCGGTAACCTCAGCA 695
 Db 415 CAGATGGCTTTTATATACGTATGATGCAACATTTGCTTCGACATCATGAACCTCAGCA 474
 Qy 696 GGCCTAATCTGCAGGACCTTCAGCTA 722
 Db 475 GACCTAGCTACAGAGATGTTCTCACTA 501
 RESULT 3
 ID AAV69887 standard; cDNA to mRNA; 954 BP.
 AC AAV69887;
 XX
 DT 10-FEB-1999 (first entry)
 DE Nucleic acid encoding a human OCIF-binding molecule (OBM).
 XX
 DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KM human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /*tag= a
 XX
 PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-Jp01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 DR WPI; 1998-594563/50.
 DR P-PSDB; AAM83018.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PS
 PS Claim 38; Page 115; 151pp; Japanese.
 CC The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence

CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 SQ Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
 Query Match 10.9%; Score 126; DB 19; Length 954;
 Best Local Similarity 72.6%; Pred. No. 5; Le-30;
 Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;
 Qy 465 CAGGACAGATTTTGGCTTAAGATGCGAATGCTGACGCTTCAACTCATCTTGTGA 524
 Db 449 CATGGTTAGATCTGGCCAAAGAGGAGCAAGCTTGAAGCTCACTTGTCTATCTCACTA 508
 Qy 525 TTATATACATCATATATCCCATGAGGCT--CATAAACGAGTCTTTCTTGTGAAACATG 582
 Db 509 TTATATGCGACCGACATCCCATCTGTTCCCATTAAGTGAAGTCTGCTCTGTAACATG 568
 Qy 583 ACCAAGATTGGGCAACGCTCTCCACATGACTTTTCAGCAGCGAAACTAAGAGTCA--- 639
 Db 569 ATCGGGGTTGGGCCAAGATCTCCACATGACTTTTACCAAGGAAACTAATAGTTAATC 628
 Qy 640 ---AAGCATTTTATTAACCGAATGCGGACATTTGCTCGACATCGGTAACCTCAGCAG 696
 Db 629 AGGATGGCTTTTATTAACCTGATGCAACATTTGCTTCGACATCATGAACCTCAGCAG 688
 Qy 697 GCCTAATCTGCAGGACCTTCAGCTA 722
 Db 689 ACCTAGCTACAGAGATGTTCTCACTA 714
 RESULT 4
 ID AAV41378 standard; cDNA; 954 BP.
 AC AAV41378;
 XX
 DT 08-OCT-1998 (first entry)
 DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 XX
 DE RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KM immune response; inflammatory response; toxic shock; sepsis;
 KM RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /*tag= a
 FT /product= "human RANKL (ligand for RANK)"
 XX
 PN WO9828426-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US23775.
 XX
 PR 14-OCT-1997; 97US-0064571.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 PI
 DR WPI; 1998-377657/32.
 DR P-PSDB; AAM69957.
 XX

PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells

PS Claim 25; Pages 59-60; 80pp; English.

CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappab (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

CC Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

XX Query Match 10.9%; Score 126; DB 19; Length 954;

XX Best Local Similarity 72.6%; Pred. No. 5.1e-30;

XX Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAAGTATTTGCTAAGATGCAATCTGACGCTCACTCATCTGTGA 524
 DB 449 CATGTTAGATCTGGCCCAAGAGAGCAAGCTTAAGCTTTTGGTCACTACTA 508
 QY 525 TTATATCATATATATCCATGAGGCT--CATAAACGAGCTTTCTTGGAAACATG 582
 DB 509 TTATATGCCACGACATCCATCTGCTCCATTAAGTAGTCTGTCCTTGGTACCATG 568
 QY 583 ACCAAGATTTGGGCAAGCTCCCAATGATGCTTACGACGAGAACTAAGATCA--- 639
 DB 569 ATCGGGGTTGGCCCAAGATCTGACATGCTTTTGAACAACTAATAGTTAATC 628
 QY 640 ---AAGCATTTATACCGAATGCGACATTTGCTCGACATGCGCAACCTCAGCAG 696
 DB 629 AGATGGCTTTTATTTACCTGATGCAACATTTTCTTTCGACATCATGAACCTTCAGGAG 688
 QY 697 GCTTAACCTTCGACGAGACCTTCAGCTA 722
 DB 689 ACCTAGCTACAGAGTATCTCAACTA 714

RESULT 5

AAV41372

ID AAV41372 standard; cDNA; 954 BP.

XX AAV41372;

DT 08-OCT-1998 (first entry)

DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..954

FT CDS /*tag- a

FT /product= "human RANKL (ligand for RANK)"

XX WO9828424-A2.

XX 02-JUL-1998.

PE 22-DEC-1997; 97WO-US23866.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

PA (IMV) IMMUNEX CORP.

PI Anderson DM, Galibert LJ, Maraskovsky E;

DR WPI: 1998-377655/32.

XX P-PSDB; AAW68293.

PT New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 59-60; 80pp; English.

CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappab (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

XX Query Match 10.9%; Score 126; DB 19; Length 954;

XX Best Local Similarity 72.6%; Pred. No. 5.1e-30;

XX Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAAGTATTTGCTAAGATGCAATCTGACGCTCACTCATCTGTGA 524
 DB 449 CATGTTAGATCTGGCCCAAGAGAGCAAGCTTGAAGCTTTCATCTCACTA 508
 QY 525 TTATATCATATATATCCATGAGGCT--CATAAACGAGCTTTCTTGGAAACATG 582
 DB 509 TTATATGCCACGACATCCATCTGCTCCATTAAGTAGTCTGTCCTTGGTACCATG 568
 QY 583 ACCAAGATTTGGGCAAGCTCCCAATGATGCTTACGACGAGAACTAAGATCA--- 639
 DB 569 ATCGGGGTTGGCCCAAGATCTGACATGCTTTTGAACAACTAATAGTTAATC 628
 QY 640 ---AAGCATTTATACCGAATGCGACATTTGCTCGACATGCGCAACCTCAGCAG 696
 DB 629 AGATGGCTTTTATTTACCTGATGCAACATTTTCTTTCGACATCATGAACCTTCAGGAG 688
 QY 697 GCTTAACCTTCGACGAGACCTTCAGCTA 722
 DB 689 ACCTAGCTACAGAGTATCTCAACTA 714

RESULT 6

AAD15311

ID AAD15311 standard; cDNA; 954 BP.

XX AAD15311;

XX 15-NOV-2001 (first entry)

DE Human receptor activator of NF kappaB ligand (RANKL) cDNA.

XX

KW Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT CDS 1..954

FT /tag= a

FT /product= "Human RANK ligand (RANKL) protein"

XX US6271349-B1.

XX 07-AUG-2001.

XX

XX 17-DEC-1998; 98US-0215649.

XX

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0077181.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0772330.

XX 07-MAR-1997; 97US-0813509.

XX 22-DEC-1997; 97US-0996139.

XX (IMNV) IMMUNEX CORP.

XX

PI Dougall WC, Galibert L;

XX

DR WPI: 2001-520313/57.

DR P-PSDB: AAE08738.

XX

XX New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as an adjunct therapy for disease characterized by neoplastic cells that express RANK

PT

PT

PT

XX Example 7; Column 69-71; 47pp; English.

XX

XX The patent discloses novel receptor activator of nuclear factor (NF)-kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of the tumour necrosis factor (TNF) receptor superfamily and associates with TNF receptor associated factor (TRAF) 2 and 3 which are important in the regulation of immune and inflammatory response. The receptors are useful for regulating immune response and in screening for inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing assays for inhibitors of signal transduction, e.g. for screening the molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful in ameliorating the negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory reactions and the effects of bone resorption. RANK acts as an anti-apoptotic signal and rescue the cells that express RANK from apoptosis. Soluble forms of the receptor are used in vivo or in vitro based screening tests for agonists or antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B activation, or to inhibit transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins

CC are useful in preparing kits for the detection of soluble RANK, or CC monitor RANK-related activity. The present sequence is a cDNA encoding CC human RANK ligand (RANKL) protein.

XX

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

SO

Query Match 10.9%; Score 126; DB 22; Length 954;

Best Local Similarity 72.6%; Pred. No. 5.1e-30;

Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAGATATTGCTAAGATGCAATCCTGACGCTCAGCTCATCTTTTA 524

DB 449 CATGGTTAGATCTGGCCAGAGAGCAAGCTTGAAGCTCTTCTCATCTCACATA 508

QY 525 TTATATCATCATATATCCCATGAGGCT--CATAAACGAGTCTTCTTGTGAACATG 582

DB 509 TTATATGCCACCGACATCCCATCTGTTCCATTAAGTAGTCTGCTTGTGATCATG 568

QY 583 ACCAAGATTGGGCAACAGCTCTCCACATGACTTTCAGCAGGAAACTAAGATCA--- 639

DB 569 ATCGGGGTGGGCCCAAGATCTCCAAACATGACTTTAGCAATGAAACTAATAGTTATC 628

QY 640 ---AAGCATTTATTAACCGGAATGCCCATTTGCTTCGACATGCGTAACTCAGCAG 696

DB 629 AGGATGGCTTTTATTTACCTGATGCCAATTTGCTTTCGACATCATGAATCTCAGGAG 688

QY 697 GCCTAATCTGACGAGACCTTCAGCTA 722

DB 689 ACCTAGCTACAGAGTATCTTCACATA 714

RESULT 7

AAD08715

ID AAD08715 standard; cDNA: 954 BP.

XX

AC AAD08715;

XX

DT 04-SEP-2001 (first entry)

XX

DE Human receptor activator of NF-chi B ligand (huRANKL) cDNA.

XX

KW Human: receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response;

KW Chromosome 18q22.1; huRANKL; chromosome 13q14; Transmembrane protein; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 1..954

FT /tag= a

FT /product= "Human RANKL protein"

XX

XX US6242213-B1.

XX

XX 05-JUN-2001.

XX

XX 22-DEC-1997; 97US-0995659.

XX

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0077181.

XX 14-OCT-1997; 97US-0064671.

XX

XX (IMNV) IMMUNEX CORP.

XX

XX Anderson DM;

XX

XX WPI: 2001-407216/43.

XX P-PSDB: AAE04426.

XX

XX New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK)

PT

XX

PS Claim 2; Column 61-64; 43pp; English.

XX The present invention relates to receptor activator of NF- χ B (RANK)

CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to

CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane

CC proteins respectively. RANK is a member of the tumour necrosis factor

CC (TNF) superfamily and it closely resembles CD40 in the extracellular

CC region. RANK associates with TNF receptor-associated factor (TRAF) 2

CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.

CC The ligands are useful for regulating immune response and in screening

CC for inhibitors of RANK. The present sequence is human RANKL (hRANKL)

CC cDNA.

XX

SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 10.9%; Score 126; DB 22; Length 954;

Best Local Similarity 72.6%; Pred. No. 5.1e-30;

Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

OY 465 CAGGAGAGTATTTCCTAGAGATGCAATCTGACGCTCAGCCCTTCAACTCATCTTGTGA 524

DB 449 CATGGTAGATCTGGCCAGAGGAGAGAGCTTGAAGCTCAGCCTTTGCTCATCTCACTA 508

OY 525 TTAATACATCAATATCCCATGAGCT--CATAAACGAGCTTTCTTTGGAACATG 582

DB 509 TTAATGCCACGACATCCCATCTGTTCCCAAAAGTGAGTGTCTCTTGGTACCATG 568

OY 583 ACCAAGATTGGGCAAGCTCTCCACATGACTTTCAGCAAGCAAGAAACTAAGAGTCA--- 639

DB 569 ATCGGGGTGGGCCAAGATCTCCACATGACTTTTACGCAATGGAAGAACTAATAGTTAATC 628

OY 640 ---AAGCATTTTATACCGGAAATGCCGACATTTGCTCTGACATCGCTAAGCTCAGAG 696

DB 629 AGGATGGCTTTTATACCTGTATGCCAATTTGCTTTCGACATCATGAACCTTCAGGAG 688

OY 697 GCCTAATCTGACGAGACCTTCAGCTA 722

DB 689 ACCTAGCTACAGAGTATCTTCACTA 714

RESULT 8

AAD05904

ID AAD05904 standard; cDNA; 954 BP.

XX

AC AAD05904;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.

XX

KW Human: receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;

KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;

KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopetrotic;

KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;

KW immune system dysfunction; familial expansile osteolysis; FEO;

KW early onset Paget's disease of bone; Ep; cytostatic; chromosome 13q14;

KW SS.

XX

OS Homo sapiens.

XX

EH Key 1 Location/Qualifiers

FT CDS 1.954

FT /"tag"= a

FT /product= "Human full-length RANKL (receptor activator

FT of NF-kappaB ligand) protein"

PN MO200136637-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000MO-US31459.

XX

PR 17-NOV-1999; 99US-0442029.

XX

PA (IMMUNEX CORP.

XX

PI Anderson DM, Hughes AE;

XX

DR WPI: 2001-329222/34.

XX

P-PSDB; AME01993.

XX

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the

PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -

XX

PS Example 7; Page 75-76; 96pp; English.

XX

CC The present invention relates to a novel receptor, referred to as RANK

CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF

CC (tumour necrosis factor) receptor superfamily. RANK is a type I

CC transmembrane protein that interacts with TNF receptor-associated

CC factors (TRAFs). Triggering of RANK by overexpression or co-expression

CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation

CC of the transcription factor NF-kappaB, a ubiquitous transcription factor

CC that is most extensively utilized in cells of the immune system.

CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating

CC negative effects of inflammatory reactions, and the effects of excess

CC bone resorption. The RANK DNAs, proteins and their analogues are useful

CC for the preparation of pharmaceutical compositions, for infecting target

CC cells for use in gene therapy applications in diagnosing diseases

CC associated with RANK, and as targets for use in screening assays. They

CC may be used in the treatment or diagnosis of immune system dysfunction.

CC The present invention also encompasses gene therapy methods to correct

CC gene-activating mutations, associated with e.g. familial expansile

CC osteolysis (FEO) and early onset Paget's disease of bone (Ep). The

CC present sequence is a cDNA encoding full-length human RANKL (hRANKL)

XX

SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 10.9%; Score 126; DB 22; Length 954;

Best Local Similarity 72.6%; Pred. No. 5.1e-30;

Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

OY 465 CAGGAGAGTATTTCCTAGAGATGCAATCTGACGCTCAGCCCTTCAACTCATCTTGTGA 524

DB 449 CATGGTAGATCTGGCCAGAGGAGAGAGCTTGAAGCTCAGCCTTTGCTCATCTCACTA 508

OY 525 TTAATACATCAATATCCCATGAGCT--CATAAACGAGCTTTCTTTGGAACATG 582

DB 509 TTAATGCCACGACATCCCATCTGTTCCCAAAAGTGAGTGTCTCTTGGTACCATG 568

OY 583 ACCAAGATTGGGCAAGCTCTCCACATGACTTTCAGCAAGCAAGAAACTAAGAGTCA--- 639

DB 569 ATCGGGGTGGGCCAAGATCTCCACATGACTTTTACGCAATGGAAGAACTAATAGTTAATC 628

OY 640 ---AAGCATTTTATACCGGAAATGCCGACATTTGCTCTGACATCGCTAAGCTCAGAG 696

DB 629 AGGATGGCTTTTATACCTGTATGCCAATTTGCTTTCGACATCATGAACCTTCAGGAG 688

OY 697 GCCTAATCTGACGAGACCTTCAGCTA 722

DB 689 ACCTAGCTACAGAGTATCTTCACTA 714

RESULT 9

ABK12877

ID ABK12877 standard; cDNA; 1945 BP.

XX

AC ABK12877;

XX

DT 18-JUN-2002 (first entry)

XX

DE cDNA encoding human TRANCE protein splice variant 2.

XX

KW Human; tumour necrosis factor-related activation induced cytokine;

KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;

(TRANC) modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, cartilage, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANC protein, splice variant 1, of the invention. TRANC is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes).

Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;

Query Match 10.9%; Score 126; DB 24; Length 2226;
Best Local Similarity 72.6%; Pred. No. 8.3e-30;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAGATTTTGTCTAAGATGCAATCTGACGCTTCACATCATCTGTGA 524
DB 605 CATGTTAGATCTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
QY 525 TTATACCATCATATATCCCATGAGCT--CATAAAGAGAGCTTTCTTCTGGAACATG 582
DB 665 TTATAGCCACGACATCCCTGCTGCTTCCATTAAGTGTCTGCTTGTACATG 724
QY 583 ACCAAGATTGGGCAAGCTCTCAACATGATCTTTCAGCAAGCAAGCAAGCAAGCA 639
DB 725 ATCGGGGTGGCCAGATCTCCCAACATGATCTTTCAGCAAGCAAGCAAGCAAGCA 784
QY 640 ---AAGCATTTATACCGGAAATGCGACATTTGCTCTGCACATGCGTAACCTGACAG 696
DB 785 AGGATGGCTTTTATACCTGATGCAACATTTGCTTGCATCATGAACTTCAGAG 844
QY 697 GCCTAAGCTGACGAGCTTCAGCTA 722
DB 845 ACCTAGCTACAGATCTTCACTA 870

RESULT 11
AA299964
ID AA299964 standard; DNA; 2271 BP.

AC AA299964;

DT 25-JUL-2000 (first entry)

XX DNA encoding a human osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW Immune response; osteoporosis; bone resorption; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 185..1138
FT /*tag= a

FT /product= "osteoprotegerin ligand"

XX WO200015807-A1.

XX 23-MAR-2000.

XX 13-SEP-1999; 99WO-DK00481.

XX 15-SEP-1998; 98DK-0001164.

XX 02-OCT-1998; 98US-0102896.
XX (MEB1-) M & E BIOTECH AS.

XX Halkier T, Haaning J;
PI WPI; 2000-271444/23.
DR P-PSDB; AAY84417.
XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT to treat, prevent and ameliorate osteoporosis -
PS Disclosure; Page 75-77; 110pp; English.

XX The present sequence encodes a human osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;

Query Match 10.9%; Score 126; DB 21; Length 2271;
Best Local Similarity 72.6%; Pred. No. 8.4e-30;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAGATTTTGTCTAAGATGCAATCTGACGCTTCACATCATCTGTGA 524
DB 633 CATGTTAGATCTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 692
QY 525 TTATACCATCATATATCCCATGAGCT--CATAAAGAGAGCTTTCTTCTGGAACATG 582
DB 693 TTATAGCCACGACATCCCTGCTGCTTCCATTAAGTGTCTGCTTGTACATG 752
QY 583 ACCAAGATTGGGCAAGCTCTCAACATGATCTTTCAGCAAGCAAGCAAGCAAGCA 639
DB 753 ATCGGGGTGGCCAGATCTCCCAACATGATCTTTCAGCAAGCAAGCAAGCAAGCA 812
QY 640 ---AAGCATTTATACCGGAAATGCGACATTTGCTCTGCACATGCGTAACCTGACAG 696
DB 813 AGGATGGCTTTTATACCTGATGCAACATTTGCTTGCATCATGAACTTCAGAG 872
QY 697 GCCTAAGCTGACGAGCTTCAGCTA 722
DB 873 ACCTAGCTACAGATCTTCACTA 898

RESULT 12
AAV70285

ID AAV70285 standard; DNA; 2274 BP.

AC AAV70285;

DT 11-FEB-1999 (first entry)

XX Human osteoprotegerin binding protein from the pcDNA/huopbpl.1insert.

XX Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 185..1138
FT /*tag= a

/product= "osteoprotegerin binding protein"

FT XX MO9846751-A1.
 PN XX
 PD 22-OCT-1998.
 XX XX
 PF 15-APR-1998; 98MO-US07584.
 XX XX
 PR 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880853.
 XX XX
 PA (AMGE-) AMGEN INC.
 XX XX
 PI Boyle WJ;
 XX XX
 DR WPI, 1998-594578/50.
 XX XX
 P-PSDB; AAMW3195.
 XX XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 XX and for diagnosis
 XX
 PS Claim 1; Fig 4; 47pp; English.
 XX XX

The present sequence encodes human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotegerin (OPG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.

Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

Query Match 10.9%; Score 126; DB 19; Length 2274;

Best Local Similarity 72.6%; Pred. No. 8.4e-30;
 Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

465 CAGGAGAAAGTATTGCTAGAAATGCAATCCGACGCTTCACCTCACTCACTTGTGTA 524
 DB 633 CATGCTTAGATCTGGCCAGAGAGACAGCTTGAAGCTTGGCTTCTCATCTACTGA 692
 OY 525 TTAATACCATCAATATCCCATGAGGCT--CATAAACGAGTCTTCTTCTTGGAAACATG 582
 DB 693 TTAATGCCAGCAGATCCCATCTGCTTCCCATTAAGTGTGCTCTTGGTACCATG 752
 OY 583 ACCAAGATGGGCAAAAGCTCTCCACATGACTTTCAGCAGCAAGAAACCTAAGAGTCA--- 639
 DB 753 ATCGGGGTGGGCAAGATCTCCACATGACTTTCAGCAATGAAACCTAAGTAAATC 812
 OY 640 ---AAGGATTTATTAACCGGAATGCCGACATTTGCTCTGCATGACGCGTAACCTCAGCAG 696
 DB 813 AGGATGGCTTTTATTAACCTGATGCAACATTTGCTTTCAGATCATGGAACCTCAGAG 872
 OY 697 GCCTAACTCTGCAGGAGCCTTCAGCTA 722
 DB 873 ACCTAGCTACAGAGATATCTTCAACTA 898

RESULT 13

ABK40274
 ID ABK40274 standard; cDNA; 2390 BP.

AC ABK40274;

DT 15-JUL-2002 (first entry)

DE cDNA encoding human PRO206 polypeptide.

KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocellular disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cytostatic; neuroprotective; gene; ss.

OS Homo sapiens.

PN WO200153486-A1.

PD 26-JUL-2001.

PF 11-FEB-2000; 2000MO-US03565.

PR 08-MAR-1999; 99MO-US05028.

PR 11-MAR-1999; 99US-123972P.

PR 11-MAY-1999; 99US-133459P.

PR 02-JUN-1999; 99MO-US12252.

PR 22-JUN-1999; 99US-140550P.

PR 20-JUN-1999; 99US-140553P.

PR 20-JUL-1999; 99US-144758P.

PR 26-JUL-1999; 99US-145698P.

PR 28-JUL-1999; 99US-146222P.

PR 17-AUG-1999; 99US-149395P.

PR 31-AUG-1999; 99MO-US20111.

PR 01-SEP-1999; 99MO-US21090.

PR 15-SEP-1999; 99MO-US28313.

PR 30-NOV-1999; 99MO-US28301.

PR 01-DEC-1999; 99MO-US28634.

PR 05-JAN-2000; 2000MO-US00219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;

PI Marsters SA, Pan J, Pilti RM, Roy MA, Smith V, Stone DM;

PI Matanabe CK, Wood WI;

XX WPI; 2002-205567/26.

DR P-PSDB; AAU86148.

XX Thirty five nucleic acids encoding PRO polypeptides, useful for

PT treating benign or malignant tumours, leukemias and lymphoid

PT malignancies, inflammatory, angiogenic and immunologic disorders -

XX Claim 50; Fig 41; 302pp; English.

XX The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The CC PRO polypeptides, agonists or anti-PRO antibodies are CC useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukemias and lymphoid malignancies, other CC disorders such as neuronal, glial, astrocytic, hypothalamic, glandular, CC macrophagal, stromal and blastocellular disorders, inflammatory, immune CC and angiogenic disorders. The polynucleotide sequences are also CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO CC polypeptides of the invention.

SO Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;

Query Match 10.9%; Score 126; DB 24; Length 2390;

Best Local Similarity 72.6%; Pred. No. 8.6e-30;
 Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

OY 465 CAGGAGAAAGTATTGCTAGAAATGCAATCCGACGCTTCACCTCACTCACTTGTGTA 524

```

Db 754 CATGGTTAGATCTGGCCAGAGAGACAGCTTGAACCTCAGCCTTTTGGCTCATCTCACTA 813
QY 525 TTAATACCATCAATATCCCATGAGGCT--CATTAACGAGTCTTTCTTGTGGAACATG 582
Db 814 TTAATGCCACCCAGATCCCTGCTGCTCCATTAAGTGAAGTCTGCTCTGTGATACATG 873
QY 583 ACCAGATTGGGCAACGCTCCACATGACTTTCAGCAAGGAAACTAAGTCA--- 639
Db 874 ATCGGGGTTGGCCCAAGATCTCCACATGACTTTAGCAATGGAAGAACTAATGATATC 933
QY 640 ---AAGGCAATTTATACCGGAATGCGGACATTTGCTCTGACATCCGTAACCTCAGCAG 696
Db 934 AGGATGGCTTTTATTAACCTGATGCAACATTTGCTTTGACATCAATGAACCTTCAGAG 993
QY 697 GCCTAAGCTCTGACAGACCTTCAGCTA 722
Db 994 ACCTAGCTACAGAGTATCTTCAACTA 1019

```

RESULT 14

AA80223
ID AA80223 standard; cDNA; 1823 BP.

XX
AC AA80223;

DT 17-AUG-1999 (first entry)

XX
DE Human TRANCE encoding cDNA.

XX
KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;

KM TNF-related activation induced cytokine; immune response; cancer;

XX
KW autoimmune disease; HIV; hypersensitivity; allergen; ds.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT CDS 1..738

FT FT /*tag= a

XX
PN WO9929865-A2.

XX
PD 17-JUN-1999.

XX
PF 14-DEC-1998; 98WO-US26486.

XX
PR 11-DEC-1998; 98US-0989479.

XX
PR 12-DEC-1997; 97US-0989479.

XX
PR 03-MAR-1998; 98US-0034099.

XX
PA (UYRQ) UNIV ROCKEFELLER.

XX
PI Choi Y, Josien R, Steinman R, Won B;

XX
DR WPI; 1999-385609/32.

XX
DR P-PSDB; AAY17873.

XX
PT TNF like proteins for treating autoimmunity and cancer

XX
PS Claim 1; Fig 1; 164pp; English.

XX
XX The present sequence encodes human TNF-related activation induced

XX
CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their

XX
CC variants, fragments, derivatives or analogues may be used as modulators

XX
CC of immune response in a mammal comprising, antisense sequences to

XX
CC TRANCE and fusion proteins comprising human and/or murine TRANCE.

XX
CC Agonists and antagonists of TRANCE, can be used to modulate immune

XX
CC response by increasing or decreasing the life span of mature dendritic

XX
CC cells and increasing or decreasing T cell activation. These techniques

XX
CC are especially useful for treating immune system related conditions such

XX
CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.

XX
CC The TRANCE polypeptides can be used to increase the viability of

XX
CC dendritic cells in vivo or in vitro, especially when used in conjunction

CC with proteins of the tumour necrosis factor (TNF) superfamily (especially

CC CD40L or TNF-alpha).

XX
SQ Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

XX
Query Match 10.6%; Score 122.8; DB 20; Length 1823;

XX
Best Local Similarity 71.8%; Pred. No. 8; le-29;

XX
Matches 191; Conservative 0; Mismatches 67; Indels 8; Gaps 2;

XX
QY 465 CAGGAGAGTATTTGCTAAGATGCAATCCGACGCTCAGCCTCAACTCATCTGTTA 524

XX
Db 233 CATGGTTAGATCTGGCCAGAGAGACAGCTTGAAGCTTACGCTTGTCTATCTACTA 292

XX
QY 525 TTAATACCATCAATATCCCATGAGGCT--CATTAACGAGTCTTTCTTGTGGAACATG 582

XX
Db 293 TTAATGCCACCCAGATCCCATCTGCTCCATTAAGTGAAGTCTGTCCTTGTGATCCATG 352

XX
QY 583 ACCAAGATTGGGCAACGCTCTCCACATGACTTTTCAGCAAGGAAACTAAGATCA--- 639

XX
Db 353 ATCGGGGCTGGGTAGATCTCCACATGACTTTTGAAGAAAGTAAAGTTAATC 412

XX
QY 640 ---AAGGCAATTTATACCGGAATGCGGACATTTGCTCTGACATCCGTAACCTCAGCAG 696

XX
Db 413 AGGATGGCTTTTATTAACCTGATGCAACATTTGCTTTGACATCATGAACCTTCAGAG 472

XX
QY 697 GCCTAAGCTCTGACAGACCTTCAGCTA 722

XX
Db 473 ACCTAGCTACAGAGTATCTTCAACTA 498

RESULT 15

AA86481
ID AA86481 standard; cDNA; 957 BP.

XX
AC AA86481;

XX
DT 29-JUN-2001 (first entry)

XX
DE Rat osteoclast differentiation factor, ODF, coding sequence.

XX
XX Rat; osteoclast formation inducer; vaccine; gene therapy;

XX
KM Osteoclast Differentiation Factor; bone; ss.

XX
OS Rattus sp.

XX
FH Key Location/Qualifiers

FT CDS 1..957

FT FT /*tag= a

XX
PN WO200123549-A1.

XX
PD 05-APR-2001.

XX
PF 29-SEP-2000; 2000WO-AU01202.

XX
PR 29-SEP-1999; 99AU-0003147.

XX
PA (UYWA-) UNIV WESTERN AUSTRALIA.

XX
PI Xu J, Zheng M;

XX
DR WPI; 2001-335526/35.

XX
DR P-PSDB; AAB82092.

XX
PT Novel nucleic acid encoding rat osteoclast differentiation factor

XX
PT useful for modulating activity of a cell, e.g., cell proliferation,

XX
PT cell differentiation and cell viability -

XX
PS Claim 1; Fig 1; 81pp; English.

XX
CC The present sequence is the coding sequence for rat Osteoclast

XX
CC Differentiation Factor (ODF). ODF is thought to be directly involved in

CC the differentiation of monocytes/macrophages into osteoclasts.
CC Osteoclasts promote dissolution of the bone matrix and solubilisation of
CC bone salts. The present sequence is useful in gene therapy, and as
CC hybridisation probes or primers. ODF protein is useful for modulating the
CC activity of cells, e.g., cell proliferation, cell differentiation and
CC cell viability, as immunogens to generate anti-rat ODF antibodies, and
CC as vaccines. Anti-rat ODF antibodies are useful in assay methods for
CC quantifying ODF polypeptides.
XX

SQ Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other:

Query Match 8.8%; Score 102; DB 22; Length 957;

Best Local Similarity 69.8%; Pred. No. 3.3e-22;

Matches 169; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

```
QY 488 GGCATCTGAGCGCTGACCTTCACATCATCTGTATTATACCATATCCCATGA 547
DB 475 GGCATGCTGAGGCTCAGCCGTTGCTCACCTCACATCATGCTGCCGACATCCCATCG 534
QY 548 GG--CTCATAAAAGAGTCTTTCTTTGGAAACATGACCAAGATTGGCAAGCTCTCC 605
DB 535 GGTCCCATAAAGTCAGTGTCTCTTGGTACCATGATCGAGGCTGGCCAGATCTCT 594
QY 606 AACATGACTTTCGCAACGAGAAACTAAGAGTCA-----AAGCATTTATTACCGGAT 659
DB 595 AACATGACGTTAAGCAACGAGAAACTAAGGTTAACCAGATGGCTTATTACCTGTAC 654
QY 660 GCCGACATTTGCTCGACATCGGTACCTCAGACAGGCCCTAAGCTGACAGACCTTCAG 719
DB 655 GCCAACATTTGCTTCAGGCAATCATGAACCTCAGGAGCGTACCTGCGACTATCTTCAG 714
QY 720 CT 721
DB 715 CT 716
```

Search completed: December 8, 2002, 17:26:08
Job time : 341.592 secs

•
•
•
•

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 16:41:40 ; Search time 2486.23 Seconds
(without alignments)
13590.225 Million cell updates/sec

Title: US-09-880-457-1
Perfect score: 1161
Sequence: 1 aaagaaggaataatcaaga.....taataaaggaaggaatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

```

Geneml: *
1:  gb_da: *
2:  gb_hcg: *
3:  gb_in: *
4:  gb_om: *
5:  gb_ov: *
6:  gb_pat: *
7:  gb_ph: *
8:  gb_pl: *
9:  gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: gb_vl: *
16: em_ba: *
17: em_fun: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rod: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_sy: *
39: em_higo_hum: *
40: em_higo_mus: *
41: em_higo_other: *

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.4	40.3	165707	2 AC104794	AC104794 Homo sapi
2	467.4	40.3	190748	9 AC010969	AC010969 Homo sapi
3	268	23.1	1186	6 AX358828	AX358828 Sequence
4	268	23.1	1186	6 AX362321	AX362321 Sequence
5	204	17.6	157250	2 AC027264	AC027264 Homo sapi
6	126	10.9	954	6 AB064268	AB064268 Homo sapi
7	126	10.9	954	9 AB061227	AB061227 Homo sapi
8	126	10.9	930	9 AB037599	AB037599 Homo sapi
9	126	10.9	954	6 AB037599	AB037599 Homo sapi
10	126	10.9	954	6 AB037599	AB037599 Homo sapi
11	126	10.9	954	6 AB037599	AB037599 Homo sapi
12	126	10.9	954	6 AB037599	AB037599 Homo sapi
13	126	10.9	954	6 AB037599	AB037599 Homo sapi
14	126	10.9	954	6 AB037599	AB037599 Homo sapi
15	126	10.9	954	6 AB037599	AB037599 Homo sapi
16	126	10.9	954	6 AB037599	AB037599 Homo sapi
17	126	10.9	954	6 AB037599	AB037599 Homo sapi
18	126	10.9	954	6 AB037599	AB037599 Homo sapi
19	126	10.9	954	6 AB037599	AB037599 Homo sapi
20	126	10.9	954	6 AB037599	AB037599 Homo sapi
21	126	10.9	954	6 AB037599	AB037599 Homo sapi
22	126	10.9	954	6 AB037599	AB037599 Homo sapi
23	126	10.9	954	6 AB037599	AB037599 Homo sapi
24	126	10.9	954	6 AB037599	AB037599 Homo sapi
25	126	10.9	954	6 AB037599	AB037599 Homo sapi
26	126	10.9	954	6 AB037599	AB037599 Homo sapi
27	126	10.9	954	6 AB037599	AB037599 Homo sapi
28	126	10.9	954	6 AB037599	AB037599 Homo sapi
29	126	10.9	954	6 AB037599	AB037599 Homo sapi
30	126	10.9	954	6 AB037599	AB037599 Homo sapi
31	126	10.9	954	6 AB037599	AB037599 Homo sapi
32	126	10.9	954	6 AB037599	AB037599 Homo sapi
33	126	10.9	954	6 AB037599	AB037599 Homo sapi
34	126	10.9	954	6 AB037599	AB037599 Homo sapi
35	126	10.9	954	6 AB037599	AB037599 Homo sapi
36	126	10.9	954	6 AB037599	AB037599 Homo sapi
37	126	10.9	954	6 AB037599	AB037599 Homo sapi
38	126	10.9	954	6 AB037599	AB037599 Homo sapi
39	126	10.9	954	6 AB037599	AB037599 Homo sapi
40	126	10.9	954	6 AB037599	AB037599 Homo sapi
41	126	10.9	954	6 AB037599	AB037599 Homo sapi
42	126	10.9	954	6 AB037599	AB037599 Homo sapi
43	126	10.9	954	6 AB037599	AB037599 Homo sapi
44	126	10.9	954	6 AB037599	AB037599 Homo sapi
45	126	10.9	954	6 AB037599	AB037599 Homo sapi

ALIGNMENTS

RESULT 1
AC104794
LOCUS
DEFINITION
Homo sapiens chromosome 2 clone RP11-254F7, WORKING DRAFT SEQUENCE,
3 unordered pieces.
AC104794
AC104794.3 GI:20340520
VERSION
HTG: HTGS_PHASE1, HTGS_DRAFT, HTGS_ACTIVEFIN.
KEYWORDS
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eultheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 165707)
Waterson, R.H.
TITLE
The sequence of Homo sapiens clone

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 3 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 COMMENT On Apr 30, 2002 this sequence version replaced gi:19339129.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 Project Information
 Center project name: H.NH0254F07

----- Summary Statistics -----
 Sequencing vector: M13; 08
 Sequencing vector: plasmid; 1008
 Chemistry: Dye-Primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 162662 bases at least Q40
 Consensus quality: 163189 bases at least Q30
 Consensus quality: 164786 bases at least Q20
 Insert size: 9479; agarose-fp
 Insert size: 167795; sum-of-contrigs
 Quality coverage: 12.78 in Q20 bases; agarose-fp
 Quality coverage: 10.53 in Q20 bases; sum-of-contrigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 3 contrigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contrigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. -----

1 1112: contrig of 1112 bp in length
 * 1113 1212: gap of unknown length
 * 1213 76227: contrig of 75015 bp in length
 * 76228 76327: gap of unknown length
 * 76328 165707: contrig of 89380 bp in length.

FEATURES
 source
 1.165707
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /clone="RP11-254F7"
 1.1112
 /note="assembly_name:Contig21"
 1213.76227
 /note="assembly_name:Contig168"
 76328.165707
 /note="assembly_name:Contig169"

BASE COUNT 42887 a 42242 c 39083 g 41295 t 200 others

Query Match 40.3%; Score 467.4; DB 2; Length 165707;
 Best Local Similarity 99.8%; Pred.No. 5.3e-134;
 Matches 468; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGAGATATTCAGAGGGCTTTTAAAGGACTTTTCCCAAGATGGAGATGAG 60
 |||||||
 Db 40150 AAAAGAGATATTCAGAGGGCTTTTAAAGGACTTTTCCCAAGATGGAGATGAG 40209

QY 61 GGAAACCTGACAGGGCTAGTCTTCTACCTCCAGCAGGACGAGTAATTCCTGAGGGAT 120
 |||||||
 Db 40210 GGAAACCTGACAGGGCTAGTCTTCTACCTCCAGCAGGACGAGTAATTCCTGAGGGAT 40269

QY 121 AAGACGCTGTTGGAGAGACATGAGGGAAGTTCTACAGAGAGCAGTGGGCTTCA 180
 |||||||
 Db 40270 AAGACGCTGTTGGAGAGACATGAGGGAAGTTCTACAGAGAGCAGTGGGCTTCA 40329

QY 181 GGAACACCTCTGAGAGGGCTGTGAGAGGGTGGGGAATCAATACCTGACCTCTCC 240
 |||||||
 Db 40330 GGAACACCTCTGAGAGGGCTGTGAGAGGGTGGGGAATCAATACCTGACCTCTCC 40389

QY 241 TTCCATCTTCCCAACCCACAGGGGTTGTGGGGCCCAAGGACCTCCCGGGGA 300
 |||||||
 Db 40390 TTCCATCTTCCCAACCCACAGGGGTTGTGGGGCCCAAGGACCTCCCGGGGA 40449

QY 301 GAGAGTGGAGAGAGGACCTGGAGAGGGCCAGTAGAAGTATCCACACAATCTTACAAG 360
 |||||||
 Db 40450 GAGAGTGGAGAGAGGACCTGGAGAGGGCCAGTAGAAGTATCCACACAATCTTACAAG 40509

QY 361 CACCAGCATTTTGTGAGCATTTGGATTGTGAGCAACAAGTCAGCAAAAAACCTTG 420
 |||||||
 Db 40510 CACCAGCATTTTGTGAGCATTTGGATTGTGAGCAACAAGTCAGCAAAAAACCTTG 40569

QY 421 CTCTGTGGAGGAGACATTTAGCAAGAAGGCAATGACACACAGTA 469
 |||||||
 Db 40570 CTCTGTGGAGGAGACATTTAGCAAGAAGGCAATGACACACAGTA 40618

RESULT 2
 AC010969/c
 AC010969/c
 DEFINITION Home sapiens BAC clone RP11-95D17 from 2, complete sequence.
 ACCESSION AC010969
 VERSION AC010969.11 GI:13677120
 KEYWORDS HTG.
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 190748)
 Sulston, J.E. and Waterston, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1097-1108 (1998)
 9847074
 2 (bases 1 to 190748)
 Sun, H., Abbott, A. and Le, T.P.
 The sequence of Homo sapiens BAC clone RP11-95D17
 Unpublished
 3 (bases 1 to 190748)
 Waterston, R.H.
 Direct Submission
 Submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 4 (bases 1 to 190748)
 Waterston, R.H.
 Direct Submission
 Submitted (19-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 5 (bases 1 to 190748)
 Waterston, R.H.
 Direct Submission
 Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 190748)
 Waterston, R.
 Direct Submission
 Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

On Apr 19, 2001 this sequence version replaced g1:11128441.

----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: MUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@wustl.edu
----- Summary Statistics
Center project name: H_NH0095D17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Teleno, M., Catanese, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-521D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17.

There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish RP11-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Size information from restriction digest suggests that the full repeat may not be represented

FEATURES

source

Location/Qualifiers
1.190748
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-95D17"
/clone_lib="RPCT-11"
185..230
/rpt_family="L2"
325..805
/rpt_family="L1"
806..1114
/rpt_family="Alu"
1449..1567
/rpt_family="MIR"
2179..2369
/rpt_family="MIR"
2626..3646
/rpt_family="L2"
3716..3745
/rpt_family="AT-rich"

repeat_region	3798..4101	/rpt_family="Alu"	EST BF770132 (NID:g12118032)"
repeat_region	4196..5255	/rpt_family="L1"	EST BF770135 (NID:g12118035)"
repeat_region	5256..5559	/rpt_family="Alu"	EST BF770127 (NID:g12118027)"
repeat_region	5560..6453	/rpt_family="L1"	EST BF770793 (NID:g12118693)"
repeat_region	6939..6989	/rpt_family="MIR"	EST BF770796 (NID:g12118696)"
repeat_region	7701..8007	/rpt_family="Alu"	EST BF770791 (NID:g12118691)"
repeat_region	8242..8532	/rpt_family="MERL-type"	
repeat_region	8533..8834	/rpt_family="Alu"	
repeat_region	8835..9300	/rpt_family="MERL-type"	
repeat_region	9322..9647	/rpt_family="L2"	
repeat_region	9652..9784	/rpt_family="MALR"	
repeat_region	9784..9848	/rpt_family="Alu"	
repeat_region	9862..10061	/rpt_family="L1"	
repeat_region	10062..10360	/rpt_family="Alu"	
repeat_region	10361..10646	/rpt_family="L1"	
repeat_region	10647..10948	/rpt_family="Alu"	
repeat_region	10949..11090	/rpt_family="L1"	
repeat_region	11135..11420	/rpt_family="Alu"	
repeat_region	11424..11704	/rpt_family="L1"	
repeat_region	11705..12015	/rpt_family="Alu"	
repeat_region	12016..12045	/rpt_family="L1"	
repeat_region	12047..12327	/rpt_family="Alu"	
repeat_region	12335..12416	/rpt_family="L1"	
repeat_region	12467..12594	/rpt_family="Alu"	
repeat_region	12596..12678	/rpt_family="L1"	
repeat_region	12698..12954	/rpt_family="Alu"	
repeat_region	12955..13065	/rpt_family="Alu"	
repeat_region	13194..13433	/rpt_family="L2"	
repeat_region	13557..13667	/rpt_family="Alu"	
misc_feature	13614..14110	/note="similar to	
misc_feature	13623..14122	/note="similar to	
misc_feature	13630..14128	/note="similar to	
misc_feature	13635..14128	/note="similar to	
misc_feature	13688..13942	/note="similar to	
misc_feature	13727..14127	/note="similar to	
misc_feature	13729..14126	/note="similar to	
repeat_region	13735..13801	/note="similar to	

misc_feature /rpl_family="MIR"
 14062..14259
 /note="similar to EST AL545813 (NID:q12878338)"
 misc_feature 14144..14259
 /note="similar to EST BF699834 (NID:q11985242)"
 misc_feature 14205..14259
 /note="similar to EST BF668191 (NID:q11942086)"
 misc_feature 14229..14259
 /note="similar to EST AL571368 (NID:q12928594)"
 misc_feature 14422..14474
 /note="similar to EST BE888644 (NID:q10345155)"
 repeat_region 14851..15156

Query Match 40.3%; Score 467.4; DB 9; Length 190748;
 Best Local Similarity 99.8%; Pred. No. 5.4e-134;
 Matches 468; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAGAGATATTCAGAGAGGCTTTCTTAAGGACTATTTCCCAAGATGGAAATGGAG 60
 Db 175455 AAAAGAGATATTCAGAGAGGCTTTCTTAAGGACTATTTCCCAAGATGGAAATGGAG 175396
 QY 61 GGAAGCTGAGGAGCTAGTGTCTACCTCCAGAGGAGAGAGCTAATTTCTGAGGGGAT 120
 Db 175395 GGAAGCTGAGGAGCTAGTGTCTACCTCCAGAGGAGAGAGCTAATTTCTGAGGGGAT 175336
 QY 121 AAGAGCTGTGTCGAGAGACATGGAGGAAAGTTCTACAGAGAGGAGAGAGGAGCTTCA 180
 Db 175335 AAGAGCTGTGTCGAGAGACATGGAGGAAAGTTCTACAGAGAGGAGAGAGGAGCTTCA 175276
 QY 181 GGAACACCTGCTTGAAGAGGCTTGAAGAGTGGGAAATCAATCTGACCTGCTTC 240
 Db 175275 GGAACACCTGCTTGAAGAGGCTTGAAGAGTGGGAAATCAATCTGACCTGCTTC 175216
 QY 241 TTCATCTCTCCCAACCCACAGAGGCTTGTGTGGGCCCCACAGAGGAGCTCCCGGGGA 300
 Db 175215 TTCATCTCTCCCAACCCACAGAGGCTTGTGTGGGCCCCACAGAGGAGCTCCCGGGGA 175156
 QY 301 GAGAAGTGGAGAGAGAGCTGGAGGAGCTAGAGGTATGACACAAATATCTACAGG 360
 Db 175155 GAGAAGTGGAGAGAGAGCTGGAGGAGCTAGAGGTATGACACAAATATCTACAGG 175096
 QY 361 CACCAAGCATTTTGTAGCATTTGGGATTTGTGACAAAGCAAGCAAAAAAAGCTTG 420
 Db 175095 CACCAAGCATTTTGTAGCATTTGGGATTTGTGACAAAGCAAGCAAAAAAAGCTTG 175036
 QY 421 CTCGTGGAGGAGCAATCTGACAAAGGAGCAATGACAAAGCAGA 469
 Db 175035 CTCGTGGAGGAGCAATCTGACAAAGGAGCAATGACAAAGCAGA 174987

RESULT 3
 AX358828 1186 bp DNA linear PAT 13-FEB-2002
 LOCUS Sequence 81 from Patent WO0193983.
 DEFINITION AX358828
 ACCESSION AX358828
 VERSION AX358828.1 GI:18675315
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secretd and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0193983-A 81 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES
 source 1..1186
 Location/Qualifiers
 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 23.1%; Score 268; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 5.9e-72;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAGATATTGCTAAGATGGCAATCCGAGGCTAGGCTTCACTCATCTGTATTAA 528
 Db 430 AGAGATATTGCTAAGATGGCAATCCGAGGCTAGGCTTCACTCATCTGTATTAA 489
 QY 529 TACCATCAATATCCCATGAGGCTCATAAAGAGCTTTCTTGTGAACATGACCAAG 588
 Db 490 TACCATCAATATCCCATGAGGCTCATAAAGAGCTTTCTTGTGAACATGACCAAG 549
 QY 589 ATTGGGCAAAAGCTCTCAACATGACTTTACGCAACGAAACCTAAGAGTCAAGGCAATT 648
 Db 550 ATTGGGCAAAAGCTCTCAACATGACTTTACGCAACGAAACCTAAGAGTCAAGGCAATT 609
 QY 649 ATTACGGGAATGCCGACATTTGCTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTGC 708
 Db 610 ATTACGGGAATGCCGACATTTGCTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTGC 669
 QY 709 AGGACCTTCAGCTATGCTGTAATTTGAG 736
 Db 670 AGGACCTTCAGCTATGCTGTAATTTGAG 697

RESULT 4
 AX362321 1186 bp DNA linear PAT 15-FEB-2002
 LOCUS Sequence 81 from Patent WO0208288.
 DEFINITION AX362321
 ACCESSION AX362321
 VERSION AX362321.1 GI:18694618
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secretd and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 81 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES
 source 1..1186
 Location/Qualifiers
 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 23.1%; Score 268; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 5.9e-72;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAGTATTGCTAAGATGGCAATCCGAGGCTAGGCTTCACTCATCTGTATTAA 528
 Db 430 AGAGTATTGCTAAGATGGCAATCCGAGGCTAGGCTTCACTCATCTGTATTAA 489
 QY 529 TACCATCAATATCCCATGAGGCTCATAAAGAGCTTTCTTGTGAACATGACCAAG 588
 Db 490 TACCATCAATATCCCATGAGGCTCATAAAGAGCTTTCTTGTGAACATGACCAAG 549
 QY 589 ATTGGGCAAAAGCTCTCAACATGACTTTACGCAACGAAACCTAAGAGTCAAGGCAATT 648
 Db 550 ATTGGGCAAAAGCTCTCAACATGACTTTACGCAACGAAACCTAAGAGTCAAGGCAATT 609
 QY 649 ATTACGGGAATGCCGACATTTGCTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTGC 708
 Db 610 ATTACGGGAATGCCGACATTTGCTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTGC 669

OY 709 AGGACCTTCAGTATGCTGAATTGAG 736
 DB 670 AGGACCTTCAGTATGCTGAATTGAG 697
 RESULT 5
 AC027264/c
 LOCUS
 DEFINITION Homo sapiens chromosome 2 clone RP11-164P8 map 2, WORKING DRAFT
 AC027264 157250 bp DNA linear HTG 24-AUG-2002
 AC027264.2 GI:10567976
 HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 157250)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Bara,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Bouckgeater,B., Brown,A., Burkett,G.,
 Campolano,A., Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S.,
 Collamore,A., Colange,M., Collins,A., Collins,S.,
 Dodge,S., Domini,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
 Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
 Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Margulis,N.,
 McCarty,M., McEwan,P., McGuire,A., McKernan,K., McNeeters,R.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testa,S., Theodore,J., Tirtell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (28-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 157250)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Bara,N., Bastien,V., Beda,F., Boguslavsky,L.,
 Bouckgeater,B., Brown,A., Burkett,G., Campolano,A., Castle,A.,
 Choepe,Y., Colangelo,M., Collins,A., Collins,S., Cooke,P.,
 Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
 Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Goyette,M.,
 Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
 Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Lacroque,K.,
 Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Margulis,N.,
 McCarty,M., McEwan,P., McGuire,A., McKernan,K., McNeeters,R.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testa,S., Theodore,J., Tirtell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 4, 2000 this sequence version replaced gi:7331634.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIDR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L8993
 Center clone name: 164.P.8
 ----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 144198 bases at least Q40
 Consensus quality: 151395 bases at least Q30
 Consensus quality: 153976 bases at least Q20
 Insert size: 15500; agarose-fp
 Insert size: 155250; sum-of-ctnigs
 Quality coverage: 4.1 in Q20 bases; agarose-fp
 Quality coverage: 4.1 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1
 901 1000: gap of 100 bp in length
 1001 2288: contig of 1288 bp in length
 2289 2388: gap of 100 bp
 2389 3949: contig of 1561 bp in length
 3950 4049: gap of 100 bp
 4050 6137: contig of 2088 bp in length
 6138 6237: gap of 100 bp
 6238 8049: contig of 1812 bp in length
 8050 8149: gap of 100 bp
 8150 12625: contig of 4476 bp in length
 12626 12725: gap of 100 bp
 12726 15710: contig of 2985 bp in length
 15711 15810: gap of 100 bp
 15811 19721: contig of 3911 bp in length
 19722 19821: gap of 100 bp
 19822 24311: contig of 4490 bp in length
 24312 24411: gap of 100 bp
 24412 32675: contig of 8264 bp in length
 32676 32775: gap of 100 bp
 32776 40400: contig of 7625 bp in length
 40401 40500: gap of 100 bp
 40501 47416: contig of 6916 bp in length
 47417 47516: gap of 100 bp
 47517 56743: contig of 9227 bp in length
 56744 56843: gap of 100 bp
 56844 64402: contig of 7561 bp in length
 64405 64504: gap of 100 bp
 64505 71871: contig of 7367 bp in length
 71872 71971: gap of 100 bp
 71972 82019: contig of 10048 bp in length
 82020 82119: gap of 100 bp
 82120 107411: contig of 25292 bp in length
 107412 107511: gap of 100 bp
 107512 116168: contig of 8657 bp in length
 116169 116268: gap of 100 bp
 116269 128458: contig of 12190 bp in length
 128459 128558: gap of 100 bp
 128559 146712: contig of 18154 bp in length
 146713 146812: gap of 100 bp
 146813 157250: contig of 10438 bp in length.
 Location/Qualifiers
 1. 157250

FEATURES
 source

```

/misc_feature      /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /chromosome="2"
                   /map="2"
                   /clone="Rp11-164P8"
                   /clone_lib="RPCT-11 Human Male BAC"
                   1..900
                   /note="assembly_fragment"
                   clone_end:SP6
                   vector_side:left"
                   1001..2288
                   /note="assembly_fragment"
                   2389..3949
                   /note="assembly_fragment"
                   4050..6137
                   /note="assembly_fragment"
                   6238..8049
                   /note="assembly_fragment"
                   8150..12625
                   /note="assembly_fragment"
                   12726..15710
                   /note="assembly_fragment"
                   15811..19721
                   /note="assembly_fragment"
                   19822..24311
                   /note="assembly_fragment"
                   24412..32675
                   /note="assembly_fragment"
                   32776..40400
                   /note="assembly_fragment"
                   40501..47416
                   /note="assembly_fragment"
                   47517..56743
                   /note="assembly_fragment"
                   56844..64404
                   /note="assembly_fragment"
                   64505..71871
                   /note="assembly_fragment"
                   71972..82019
                   /note="assembly_fragment"
                   82120..107411
                   /note="assembly_fragment"
                   107512..116168
                   /note="assembly_fragment"
                   116269..128458
                   /note="assembly_fragment"
                   128559..146712
                   /note="assembly_fragment"
                   146813..157250
                   /note="assembly_fragment"
                   clone_end:77
                   vector_side:right"
BASE COUNT      45395 a 32097 c 31766 g 45991 t 2001 others
ORIGIN
Query Match      17.6% Score 204; DB 2; Length 157250;
Best Local Similarity 95.5% Pred. No. 9.8e-52;
Matches 210; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 942 CATAGTTTGAAGCAAGGATTTGATTTGTGATGAATGTTGTGTTCACTGAAG 1001
    |||||
DB 149305 GTTATGTTTGAATTCATAGGATTTGCAATTTGTGATGAATGTTGTGTTCACTGAAG 149246
    |||||
QY 1002 CTGAAGTTGTAACCTGTAACCAAGAGACATGATGATGTTCTTCTCACTAAATG 1061
    |||||
DB 149245 CTGAAGTTGTAACCTGTAACCAAGAGACATGATGATGTTCTTCTCACTAAATG 149186
    |||||
QY 1062 GCAATGTCCTTGAGAGAAGCCCTGCTTAATCATCTCTGTCCTCAAGCCTGGCTTAATC 1121
    |||||
DB 149185 GCAATGTCCTTGAGAGAAGCCCTGCTTAATCATCTCTGTCCTCAAGCCTGGCTTAATC 149126
    |||||
QY 1122 ATATGCTTATCGCATGCTTTTAATAAAGAGAAATATGC 1161
    |||||

```

DB 149125 ATATGCTTATCGCATGCTTTTAATAAAGAGAAATATGC 149086

```

RESULT 6
AB064268
LOCUS
DEFINITION
Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor
kappa B ligand 3, complete cds.
AB064268
AB064268.1 GI:18143616
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens cDNA to mRNA.
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Ikedo,T., Kuroyama,H. and Hirokawa,K.
Determination of human RANKL isoforms
2 (bases 1 to 818)
Ikedo,T. and Kuroyama,H.
Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Immunology, Graduate
School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail:toru.ph2@med.tmd.ac.jp, Tel:81-3-5803-5176,
Fax:81-3-5803-0123)
Location/Qualifiers
1..818
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..818
/gene="hRANKL 3"
84..818
/gene="hRANKL 3"
/codon_start=1
/product="receptor activator of nuclear factor kappa B
ligand 3"
/protein_id="BAB79693.1"
/db_xref="GI:18143617"

```

```

FEATURES
source
1..818
/gene="hRANKL 3"
84..818
/gene="hRANKL 3"
/codon_start=1
/product="receptor activator of nuclear factor kappa B
ligand 3"
/protein_id="BAB79693.1"
/db_xref="GI:18143617"

```

```

BASE COUNT      243 a 173 c 184 g 218 t
ORIGIN
Query Match      10.9% Score 126; DB 9; Length 818;
Best Local Similarity 72.6% Pred. No. 1.3e-27;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;
QY 465 CAGGAGAACTATTTGCTAAGATGCAATCTCAGAGCTCAGCCTCAATCTTGTGA 524
    |||||
DB 313 CATGTTAAGATCTGGCCCAAGAGAGCAAGCTTGAAGCTCAGCCTTGGCTATCTCACA 372
    |||||
QY 525 TTAATACCATTAATCCCATGAGGCT--CATTAACAGAGCTTTCTTCTTGGAAACATG 582
    |||||
DB 373 TTAATGCCACGCAATCTCCATCTGGTCCCAATGAAGTAGTGTCTCTTGTGACCATG 432
    |||||
QY 583 ACCAAGATTGGCAACGCTCTCAACATGACTTTCAGCAAGCAAGCAAACTAAGAGTCA 639
    |||||
DB 433 ATCGGGGTTGGCCCAAGATCTCCCAACATGACTTTTACGAATGGAATACTAATGTTAATC 492
    |||||
QY 640 ---AAGCATTTATTAACCGGAATGCCAGACTTTGCTTCGACATGCGTAACCTCAGCAG 696
    |||||
DB 493 AGGATGGCTTTTATTAACCTGTATGCCAATTTGCTTTCGACATCATGAATCTCAGAG 552
    |||||
QY 697 GCCTAATCTGCAAGAGACTTCAGCTA 722
    |||||
DB 553 ACCTAGCTACAGAGTATCTTCACTA 578
    |||||

```

```

RESULT 7
AB061227          911 bp  mRNA  linear  PRI 03-NOV-2001
LOCUS             Homo sapiens mRNA for hRANKL 2, complete cds.
DEFINITION        AB061227.1 GI:16610212
ACCESSION         AB061227.1 GI:16610212
VERSION           AB061227.1 GI:16610212
KEYWORDS          Homo sapiens cDNA to mRNA.
SOURCE            Homo sapiens
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE         1 Ikeda,T., Kuroyama,H. and Hirokawa,K.
AUTHORS           Human RANKL isoform
JOURNAL           Unpublished
TITLE             2 (bases 1 to 911)
AUTHORS           Ikeda,T. and Kuroyama,H.
AUTHORS           Direct Submission
TITLE             Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical
JOURNAL           and Dental University, Pathology and Immunology, 1-5-45 Yushima,
                  Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: tohru.pth2@med.tmd.ac.jp,
                  Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES          Location/Qualifiers
                  1..911
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  99..911
                  /codon_start=1
                  /product="hRANKL 2"
                  /protein_id="BAB71768.1"
                  /db_xref="GI:16610213"
                  /translation="MFVALIGLGIGVGVSALEFFYRAQMDPNRISDGTGHCIRYL
                  RLHENAFQDITLESODTKLIPDSCRIRKQAFQAVOKELOHIVGSOHIAEKAMVNG
                  SHLDIAKRKLEAOPFAHLINATDIPSGSHKYSLSMYHGRMAKISNMTFSKRLI
                  VNODGFYLYANICPRHETSGDIAEYIOLMYVYKTSIKITSSHTLMKGSTKIVS
                  GNSERHFYSINVGFFKLRSCEISTIEVSNPSLDDPDQDATTGAFKVRDID"
BASE COUNT       253 a 211 c 217 g 230 t
ORIGIN
Query Match      10.9%; Score 126; DB 9; Length 911;
Best Local Similarity 72.6%; Pred. No. 1.3e-27;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAGTAATTTGCTAAGATGCAATCTGACGCTCAGCCTTCAACTCATCTTGTGA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 CATGGTTATCATCTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TTAATACCATCAATATCCATGAGGCT--CATAAACGAGTCTTTCTTCTTGGAACATG 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 TTAATGCCACCGACATCCATCTGTTCCATTAAGTAGAGTGTCTCTTGGTACCATG 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 583 ACCAAGATTGGGCAAAAGCTCTCCACATGACTTTGACGACGGAACCTAAGAGTCA--- 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 ATCGGGGTTGGGCAAGATCTCCACATGACTTTTAGCAATGGAACCTAATAGTTATC 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 ---AAGCATTTATTAACCGAATGCCGACATTTGCTCTGCACATCGGTAACCTCAGAG 696
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 AGGATGGCTTTTATTAACCGTATGATGCAACATTTGCTTGCACATGAAACCTCAGAG 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 697 GCCTAAGCTCGAGGAGCTTCAGCTA 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 646 ACCTAGCTACAGAGTATCTTCAACTA 671

```

```

RESULT 8
AB037599          930 bp  mRNA  linear  PRI 19-MAR-2002
LOCUS             Homo sapiens mRNA for SODF/TRANCE, complete cds.
DEFINITION        AB037599.1 GI:6663047
ACCESSION         AB037599.1 GI:6663047
VERSION           AB037599.1 GI:6663047
KEYWORDS          Homo sapiens male tongue epithelial-like squamous cell carcinoma
                  cell_line:SCC-4 cDNA to mRNA.

```

```

ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE         1 Nagai,M., Kyakumoto,S. and Sato,N.
AUTHORS           Cancer cells responsible for humoral hypercalcemia express mRNA
                  encoding a secreted form of ODF/TRANCE that induces osteoclast
                  formation
JOURNAL           Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)
MEDLINE           20175237
REFERENCE         2 (bases 1 to 930)
AUTHORS           Nagai,M., Kyakumoto,S. and Sato,N.
AUTHORS           Direct Submission
TITLE             Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University
JOURNAL           School of Dentistry, Department of Biochemistry, 19-1 Uchimaru,
                  Morioka, Iwate 020-8505, Japan (E-mail: magai@iwate-med.ac.jp,
                  Tel:+81-19-651-5111 (ex.4436), Fax:+81-19-654-4147)
FEATURES          Location/Qualifiers
                  1..930
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /sex="male"
                  /cell_line="SCC-4"
                  /tissue_type="epithelial-like squamous cell carcinoma"
                  /tissue_type="tongue"
                  1..930
                  /gene="sodf/trance"
                  /gene="sodf/trance"
                  95..829
                  /codon_start=1
                  /product="SODF/TRANCE"
                  /protein_id="BA90488.1"
                  /db_xref="GI:6663048"
                  /translation="MDPNRISDGTGHCIRYLRLHNAFDQITLESODTKLIPDSCR
                  RIKQAFQAVOKELOHIVGSOHIAEKAMVNGSHLDIAKRKLEAOPFAHLINATDIP
                  SGSHKYSLSMYHGRMAKISNMTFSNKLIVNODGFYLYANICPRHETSGDIAEYIOLMYVYKTSIKIT
                  SSHTLMKGSTKIVS GNSERHFYSINVGFFKLRSCEISTIEVSNPSLDDPDQDATTGAFKVRDID"
BASE COUNT       283 a 184 c 200 g 260 t 3 others
ORIGIN
Query Match      10.9%; Score 126; DB 9; Length 930;
Best Local Similarity 72.6%; Pred. No. 1.3e-27;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAGTAATTTGCTAAGATGCAATCTGACGCTCAGCCTTCAACTCATCTTGTGA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 324 CATGGTTATCATCTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TTAATACCATCAATATCCATGAGGCT--CATAAACGAGTCTTTCTTCTTGGAACATG 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 384 TTAATGCCACCGACATCCATCTGTTCCATTAAGTAGAGTGTCTCTTGGTACCATG 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 583 ACCAAGATTGGGCAAAAGCTCTCCACATGACTTTGACGACGGAACCTAAGAGTCA--- 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 444 ATCGGGGTTGGGCAAGATCTCCACATGACTTTTAGCAATGGAACCTAATAGTTATC 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 ---AAGCATTTATTAACCGAATGCCGACATTTGCTCTGCACATCGGTAACCTCAGAG 696
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 504 AGGATGGCTTTTATTAACCGTATGATGCAACATTTGCTTGCACATGAAACCTCAGAG 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 697 GCCTAAGCTCGAGGAGCTTCAGCTA 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 564 ACCTAGCTACAGAGTATCTTCAACTA 589

```

```

RESULT 9
ARI56434          954 bp  DNA  linear  PAT 08-AUG-2001
LOCUS             ARI56434
DEFINITION        Sequence 12 from patent US 6242213.
ACCESSION         ARI56434
VERSION           ARI56434.1 GI:15125138
KEYWORDS          ARI56434.1 GI:15125138

```


SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 954)
AUTHORS Anderson, D.M.
TITLE Isolated DNA molecules encoding RANK-L
JOURNAL Patent: US 6242213-A 12 05-JUN-2001;
FEATURES Location/Qualifiers
source 1..954
/organism="unknown"

BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 10.9%; Score 126; DB 6; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.3e-27;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAAGTATTGCTAAGATGGCAATCCCTGACGCTTCAGCTTCACATCTTGTGA 524
DB 449 CATGGTTAGATCTGGCCAGAGAGCAAGCTTGAAGCTTCAGCTTTCCTCATCTCAGTA 508
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAAGAGTCTTCTTCTTGGAACATG 582
DB 509 TTATGCGACCGACATCCCATCTGTTCCCATAAAGTAGTGTCTCTCTGGTACCATG 568
QY 583 ACCAAGATTGGGCAAACTCTCCAAACATGACTTTAGCAACGAGAAACTAAGAGTCA--- 639
DB 569 ATCGGGGTTGGGCCAAGATCTCCAAACATGACTTTAGCAATGAGAAACTAATAGTTAATC 628
QY 640 ---AAGGCATTATTACGGAGATGCCGACATTTGCTCTGACATCGGTAACCTCAGCAG 696
DB 629 AGATGGCTTTTATTACTGTAATGCCACATTTGCTTTGACATCATGAACCTCAGGAG 688
QY 697 GCCTAACTCTGCAGGACCTTCAGCTA 722
DB 689 ACCTAGCTACAGAGTATCTTCAACTA 714

RESULT 10
ARI64148
LOCUS ARI64148 954 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 12 from patent US 6271349.
ACCESSION ARI64148
VERSION ARI64148.1 GI:16235114
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 954)
AUTHORS Dougall, W.C. and Galibert, L.
TITLE Receptor activator of NF- κ B
JOURNAL Patent: US 6271349-A 12 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..954
/organism="unknown"

BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 10.9%; Score 126; DB 6; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.3e-27;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAAGTATTGCTAAGATGGCAATCCCTGACGCTTCAGCTTCACATCTTGTGA 524
DB 449 CATGGTTAGATCTGGCCAGAGAGCAAGCTTGAAGCTTCAGCTTTCCTCATCTCAGTA 508
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAAGAGTCTTCTTCTTGGAACATG 582
DB 509 TTATGCGACCGACATCCCATCTGTTCCCATAAAGTAGTGTCTCTGGTACCATG 568
QY 583 ACCAAGATTGGGCAAACTCTCCAAACATGACTTTAGCAACGAGAAACTAAGAGTCA--- 639
DB 569 ATCGGGGTTGGGCCAAGATCTCCAAACATGACTTTAGCAATGAGAAACTAATAGTTAATC 628

QY 640 ---AAGGCATTATTACCGGAATGCCGACATTTGCTCTGACATCGGTAACCTCAGCAG 696
DB 629 AGATGGCTTTTATTACTGTAATGCCACATTTGCTTTGACATCATGAACCTCAGGAG 688
QY 697 GCCTAACTCTGCAGGACCTTCAGCTA 722
DB 689 ACCTAGCTACAGAGTATCTTCAACTA 714

RESULT 11
AX147989
LOCUS AX147989 954 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 12 from Patent WO0136637.
ACCESSION AX147989
VERSION AX147989.1 GI:14346964
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 954)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Receptor activator of nf- κ B
JOURNAL Patent: WO 0136637-A 12 25-MAY-2001;
Immunex Corporation (US)
FEATURES Location/Qualifiers
source 1..954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="unnamed protein product"

CDS
/codon_start=1
/protein_id="CAC41185.1"
/db_xref="GI:14346965"
/translation="MRASRDYKYLKSGHEMGPGAPHEGPLHAPPPAPHPAPPA
SRMEVALGLGQVVCVAFEPFPAQDPMRISDGTICIRILRHNAFODT
TLESODTKLIPDSCRIRKQAFQGAQVOKHIVGSOHRAEKAMVDSDLDARSKL
EAQPRALHITNMTDITSGSHKYSLSMTHDRGAKISNMFEKGLIVNDGPFYLYA
NICFRHETSGDLATETLDIMVTVYTKISITIPSSHITLMKGGSTYWGNSLFFHYSIN
VGGFRLRSGEISLIVSNPSLDPQDQATYFGAFKVRDID"

BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 10.9%; Score 126; DB 6; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.3e-27;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAAGTATTGCTAAGATGGCAATCCCTGACGCTTCAGCTTCACATCTTGTGA 524
DB 449 CATGGTTAGATCTGGCCAGAGAGCAAGCTTGAAGCTTCAGCTTTCCTCATCTCAGTA 508
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAAGAGTCTTCTTCTTGGAACATG 582
DB 509 TTATGCGACCGACATCCCATCTGTTCCCATAAAGTAGTGTCTCTGGTACCATG 568
QY 583 ACCAAGATTGGGCAAACTCTCCAAACATGACTTTAGCAACGAGAAACTAAGAGTCA--- 639
DB 569 ATCGGGGTTGGGCCAAGATCTCCAAACATGACTTTAGCAATGAGAAACTAATAGTTAATC 628
QY 640 ---AAGGCATTATTACCGGAATGCCGACATTTGCTCTGACATCGGTAACCTCAGCAG 696
DB 629 AGATGGCTTTTATTACTGTAATGCCACATTTGCTTTGACATCATGAACCTCAGGAG 688
QY 697 GCCTAACTCTGCAGGACCTTCAGCTA 722
DB 689 ACCTAGCTACAGAGTATCTTCAACTA 714

RESULT 12
AX451895
LOCUS AX451895 954 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 5 from Patent WO0224896.

Accession	AX451895	GI:21698735
Version	AX451895.1	
Keywords		
Source	human.	
Organism	Homo sapiens	
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.	
Reference Title	1	
Journal	Douglall, W.C.	
Features	Screening assays for agonists or antagonists of receptor activat or of nF-kB Patent: WO 0224896-A 5 28-MAR-2002; IMMUNEX CORPORATION (US) Location/Qualifiers 1..954 /organism="Homo sapiens" /db_xref="taxon:9606" 1..954 /note="unnamed protein product" /codon_start=1 /protein_id="CAD37794.1" /db_xref="gi:21698735" /translation="MRASRDYIKYLGSSEMGSGPAPHKGPLHAPPAPHPAPAA SRSMVALGIGLQVVSVALFFYPFAOMDPNRIISDGTICIRILRLHNAFOPT TLESQDRLIPDSCKRIKQAFQAVOKELHIVGSSQIRAEKAVDGSWIDAKRSKL EAQFPALHILNATDIPSGSHKVSLSMYHDEGAKIKSNMPEFNKLIYNODGFYLYA NICRHHETSDLALEYTOLMIVYTKTSIKIPSSHTLMKGGSTYWGNSBFFHYSIN VGGFKLRSSEISIEVSNPSLDDPDATFFGAFKVIDD"	
BASE COUNT	255 a 239 c 227 g 233 t	
ORIGIN		
Query Match	10.9%; Score 126; DB 6; Length 954;	
Best Local Similarity	72.6%; Pred. No. 1.3e-27;	
Matches 193; Conservative	0; Mismatches 65; Indels 8; Gaps 2;	
Y	465 CAGGAGAGTATTTCCTAAGAATGCAATTCCTGACGCTCAGCCCTTCAATCATCTTTGTA 524	
Db	449 CATGTTTGATCTGGCCAGAGAGCAAGCTTGAAGCTTCACCTTTGCTCATCTCACA 508	
Y	525 TTAATACCATCAATATCCCATGAGGCT--CATTAACAGAGCTTCTCTGTTGGAACATG 582	
Db	509 TTAATGCCACCGACATCCCATCTGTTGCCATTAAGTAGAGTCTGTCTCTGTGATCATG 568	
Y	583 ACCAAGATTGGGCAACAGCTCTCCAACTGACTTTGACGACGAAACTAAGAGTCA--- 639	
Db	569 ATCGGGGTTGGGCCAAGATCTCCAACTGACTTTGACGAAATGAAACTAATAGTTATC 628	
Y	640 ---AAGCATTTATTACCGGAATGCCACATTCCTCTCGACATCGCGTAACTCAGAC 696	
Db	629 AGAATGGCTTTTATTACTGTAATGCCAACATTTCTTTGACATCATGAAACTTCAGAG 688	
Y	697 GCGTAATCTGCGACGACCTTCAGTA 722	
Db	689 ACTGACTACAGATATCTTCAACTA 714	
RESULT 13		
AB064270		
LOCUS	AB064270	
DEFINITION	Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear	
ACCESSION	AB064270	
VERSION	AB064270.1	
KEYWORDS	GI:18143620	
SOURCE		
ORGANISM	Homo sapiens cDNA to mRNA.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.	
JOURNAL	Ikeda, T., Kuroyama, H. and Hirokawa, K.	
REFERENCE	1	
JOURNAL	Determination of human RANKL isoforms	
REFERENCE	2 (bases 1 to 972)	

AUTHORS		TITLE		JOURNAL		FEATURES	
Ikeda, T. and Kuroyama, H.		Direct Submission		Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: tohru.ph2@med.tmd.ac.jp, Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)		Location/Qualifiers	
source		1..972		/organism="Homo sapiens"		/db_xref="taxon:9606"	
gene		1..972		/gene="hRANKL 2-2"		/db_xref="GI:18143621"	
CDS		160..972		/gene="hRANKL 2-2"		/codon_start=1	
		/product="receptor activator of nuclear factor kappa B ligand 2-2"		/protein_id="BAB79695.1"		/translation="MEVALIGIGGVVCSALPFPYAFKADPNRISDGTGHCYRITRIILHLEHADPDPTLIESDPTKPLIPDSRRIRKQAFQGVQLELIVGSQHI RAEKAWDVSMLDKRSKLEAEFPFALITINATDIPSGSHKVSLSMYHQRMAKLSNMFNSGKLVNODGFYLVANICFPRHETSGDLATEFLQMYVYTKSIRIPSSHITLMKGSGRYWGNSERHFYSINVGFFKLRSGSEISIEVSNPSILDDPDATYFGAFKVIDID"	
BASE COUNT		270 a 219 c 249 g 234 t					
ORIGIN							
Query Match		10.9%		Score 126;		DB 9; Length 972;	
Best Local Similarity		72.6%		Pred. No. 1.3e-27;			
Matches 193:		Conservative		0; Mismatches 65;		Indels 8; Gaps 2;	
QY	465 CAGGAGAACTATTGCTGTAGAATGCAATCCGACGCTCAGCCTCACTCATCTGTGA	524					
Db	467 CATGGTTAGATCTGGCCAAAGAGAGCAAGCTTGAAGCTCAGCTTTGCTCATCTCACTA	526					
QY	525 TTAATACCATCAATATCCCATGAGCT--CATAAACGAGTCTTTCTTGGAACATG	582					
Db	527 TTAATGCCACGACATCCCATCTGGTTCCCATAAAGTAGTGTCTCTTGTCATCATG	586					
QY	583 ACCAAGATTGGCAACACTCTCCACATGACTGACTTCAGCAGCAAGAAACTAAGAGTCA---	639					
Db	587 ATCGGGGTTGGGCCCAAGATCTCCACATGACTTTTACGAATGGAATACTAATAGTTAATC	646					
QY	640 ---AAGCATTATTTACCGGAATGCCGCAATTTGGCTCTCGACATGCGCTAACCTCAGCAG	696					
Db	647 AGGAGGCTTTTATTTACCTGTATGCAACATTTGGCTTCGACATCATGAACCTTCAGCAG	706					
QY	697 GCGTACCTCGAGAGACCTTAGCTA 722						
Db	707 ACGTAGCTACAGAGATATCTCAACTA 732						
RESULT 14		AB064269		1034 bp		mRNA linear	
LOCUS		AB064269		Homo sapiens hRANKL 1 mRNA for receptor activator of nuclear factor		PRI 26-DEC-2001	
DEFINITION		hRANKL 1 mRNA for receptor activator of nuclear factor					
ACCESSION		AB064269		complete cds.			
VERSION		AB064269.1		GI:18143618			
KEYWORDS							
SOURCE		Homo sapiens		Homo sapiens			
ORGANISM		Homo sapiens		Homo sapiens			
REFERENCE		1 Ikeda, T., Kuroyama, H. and Hirokawa, K.		Determination of human RANKL isoforms			
AUTHORS		Ikeda, T. and Kuroyama, H.		Direct Submission			
TITLE		Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental					

University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail: toru.pch2@med.tmd.ac.jp, Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)

Location/Qualifiers

1.1034

/organism="Homo sapiens"

/db_xref="taxon:9606"

1.1034

/gene="hRANKL 1"

81.1034

/gene="hRANKL 1"

/codon_start=1

/product="receptor activator of nuclear factor kappa B

ligand 1"

/protein_id="BAB79694.1"

/db_xref="GI:18143619"

/translation="MRASRDYTKYLRGSEMGGPGAPHEGLHAPPPAPHPAPPA

SRSMFVALIGLGQVVCYALFFFRADMPNRISEDTHCYRILRLHENAADODT

TLESQDTKLIPDSCRIRKQAFQAVQKELQIVSQHRAKAMVDSWLDLAKRSKL

EAQPFALHTINATDIPSGSHKVSLSWYHDKWAKISMTESNGKLIYNODGFYLYA

NICFRHETSGDLATEYLQIMVYVTKTSIKIPSSHTLMKGSSTKYWSGNSSEHFYSIN

VGGFELRSGEELISIEVSNPSLDDPDATYFGAFKVRDID"

BASE COUNT 275 a 257 c 265 g 237 t

ORIGIN

Query Match 10.9%; Score 126; DB 9; Length 1034;

Best Local Similarity 72.6%; Pred. No. 1.3e-27;

Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

465 CAGGAGAGATTTGTAAGATGCAATCCGACGCTGACGCTTCAATCATCTTGTGA 524

DB 529 CAGGTGATGATCTGCGCAAGAGAGCAAGCTTGAAGCTTGTGCTCATCTCACTA 588

525 TTATACCATCAATATCCATGAGCT--CATAAACGAGCTTTCTTGTGAAACATG 582

DB 589 TTATATGCCACGACATCCATCTGCTCCATAAAGTAGTGTCTCTTGTGATACATG 648

583 ACCAAGATTGGGCAACGCTCCCAATGACATTCAGCAAGCAAACTAAGAGTCA--- 639

DB 649 ATCGGGGTTGGGCCAAGATCTCCACATGACTTTTACCAATGAAACCTAATAGTTATC 708

640 ---AAGCATTTATTTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGCAG 696

DB 709 AGGATGGCTTTTATCTGATATGCCACATTTGCTTGCACATCAATGAAACTCAGAGAG 768

697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 769 ACCTAGCTACAGAGTATCTTCAACTA 794

RESULT 15

AF019047 2201 bp mRNA linear PRI 22-NOV-1997

LOCUS AF019047

DEFINITION Homo sapiens receptor activator of nuclear factor kappa B ligand

(RANKL) mRNA, complete cds.

ACCESSION AF019047

VERSION AF019047.1 GI:2612921

KEYWORDS

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2201)

AUTHORS Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.,

Tometsko, M.E., Roux, E.R., Teepe, M.C., Dubose, R.F., Cosman, D. and

Galibert, L.

TITLE A homologue of the TNF receptor and its ligand enhance T-cell

growth and dendritic-cell function

JOURNAL Nature 390 (6656), 175-179 (1997)

MEDLINE 98032977

PUBMED 9367155

REFERENCE 2 (bases 1 to 2201)

AUTHORS

Anderson, D.M., Billingsley, W., Dougall, W., Maraskovsky, E.,

Cosman, D., Dubose, R., and Galibert, L.

TITLE Direct Submission Molecular Biology, Immunex Corp., 51

JOURNAL Submitted (13-AUG-1997)

University St., Seattle, WA 98101, USA

Location/Qualifiers

1.2201

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="13"

/map="13q14"

1.2201

/gene="RANKL"

129.1082

/gene="RANKL"

/note="receptor activator of nuclear factor kappa B

ligand"

/codon_start=1

/product="RANKL"

/protein_id="BAB86811.1"

/db_xref="GI:2612922"

/translation="MRASRDYTKYLRGSEMGGPGAPHEGLHAPPPAPHPAPPA

SRSMFVALIGLGQVVCYALFFFRADMPNRISEDTHCYRILRLHENAADODT

TLESQDTKLIPDSCRIRKQAFQAVQKELQIVSQHRAKAMVDSWLDLAKRSKL

EAQPFALHTINATDIPSGSHKVSLSWYHDKWAKISMTESNGKLIYNODGFYLYA

NICFRHETSGDLATEYLQIMVYVTKTSIKIPSSHTLMKGSSTKYWSGNSSEHFYSIN

VGGFELRSGEELISIEVSNPSLDDPDATYFGAFKVRDID"

BASE COUNT 658 a 429 c 497 g 617 t

ORIGIN

Query Match 10.9%; Score 126; DB 9; Length 2201;

Best Local Similarity 72.6%; Pred. No. 1.4e-27;

Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

465 CAGGAGAGATTTGTAAGATGCAATCCGACGCTGACGCTTCAATCATCTTGTGA 524

DB 577 CAGGTGATGATCTGCGCAAGAGAGCAAGCTTGAAGCTTGTGCTCATCTCACTA 636

525 TTATACCATCAATATCCATGAGCT--CATAAACGAGCTTTCTTGTGAAACATG 582

DB 637 TTATATGCCACGACATCCATCTGCTCCATAAAGTAGTGTCTCTTGTGATACATG 696

583 ACCAAGATTGGGCAACGCTCCCAATGACATTCAGCAAGCAAACTAAGAGTCA--- 639

DB 697 ATCGGGGTTGGGCCAAGATCTCCACATGACTTTTACCAATGAAACCTAATAGTTATC 756

640 ---AAGCATTTATTTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGCAG 696

DB 757 AGGATGGCTTTTATCTGATATGCCACATTTGCTTGCACATCAATGAAACTCAGAGAG 816

697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722

DB 817 ACCTAGCTACAGAGTATCTTCAACTA 842

QY 697 GCCTAATCTGACAGACCTTCAGCTA 722